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OM protein - protein search, using sw model

Run on: August 9, 2004, 13:27:45 ; Search time 18 Seconds
(without alignments)
37.285 Million cell updates/sec

Title: US-09-277-074-9
Perfect score: 74
Sequence: 1 TPPAYRPNAPIL 13

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS COMB pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	13	1	US-08-305-871A-14
2	74	100.0	13	4	US-08-464-496-19
3	74	100.0	13	4	US-08-788-822A-16
4	74	100.0	13	4	US-08-197-484-113
5	74	100.0	13	4	US-09-311-784A-49
6	74	100.0	13	4	US-09-664-945-50
7	74	100.0	13	5	PCT-US92-07218-19
8	74	100.0	13	5	PCT-US95-02121-113
9	74	100.0	13	5	PCT-US95-16415-9
10	74	100.0	14	4	US-09-311-784A-124
11	74	100.0	15	3	US-08-737-896-7
12	74	100.0	15	5	PCT-US96-09951-7
13	74	100.0	21	5	US-09-100-409A-45
14	74	100.0	21	5	PCT-US95-13841-13
15	74	100.0	23	4	US-08-464-496-20
16	74	100.0	23	4	US-08-197-484-114
17	74	100.0	23	5	PCT-US92-07218-20
18	74	100.0	23	5	PCT-US95-02121-114
19	74	100.0	26	4	US-08-464-496-21
20	74	100.0	26	4	US-08-197-484-115
21	74	100.0	26	5	PCT-US92-07218-21
22	74	100.0	26	5	PCT-US95-02121-115
23	74	100.0	80	4	US-09-311-784A-22
24	74	100.0	118	4	US-09-311-784A-8
25	74	100.0	119	4	US-09-311-784A-10
26	74	100.0	136	4	US-09-311-784A-12
27	74	100.0	138	4	US-09-311-784A-4

28	74	100.0	152	4	US-09-311-784A-20
29	74	100.0	154	3	US-08-968-747-1
30	74	100.0	155	3	US-08-968-747-17
31	74	100.0	159	3	US-08-445-585-3
32	74	100.0	161	3	US-08-968-747-19
33	74	100.0	164	4	US-09-311-784A-18
34	74	100.0	183	3	US-08-968-747-20
35	74	100.0	183	3	US-09-248-588-2
36	74	100.0	183	3	US-09-248-588-4
37	74	100.0	183	5	PCT-US96-10602-12
38	74	100.0	185	1	US-07-739-642-2
39	74	100.0	185	1	US-07-739-642-4
40	74	100.0	185	1	US-07-739-642-8
41	74	100.0	185	1	US-07-739-642-10
42	74	100.0	185	1	US-07-739-643-2
43	74	100.0	185	1	US-07-739-643-4
44	74	100.0	185	1	US-07-739-643-6
45	74	100.0	185	1	US-07-739-643-10

ALIGNMENTS

RESULT 1
US-08-305-871A-14
; Sequence 14, Application US/08305871A
; Patent No. 5736142
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Grey, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffrey L.
; TITLE OF INVENTION: Alteration of Immune Response Using Pan
; TITLE OF INVENTION: DR-Binding Peptides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,871A
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,101
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-0062-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-305-871A-14

Query Match 100.0%; Score 74; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
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DB 1 TPPAYRPPNAPIL 13

RESULT 2
US-08-464-496-19
; Sequence 19, Application US/08464496
; Patent No. 6322789
; GENERAL INFORMATION:
; APPLICANT: Eptimmune, Inc.
; APPLICANT: Vitello, Maria
; APPLICANT: Chesnut, Robert
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; TITLE OF INVENTION: EPTOPE
; FILE REFERENCE: 39963-20001.13
; CURRENT APPLICATION NUMBER: US/08/464,496
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 07/935,811
; PRIOR FILING DATE: 1992-08-26
; PRIOR APPLICATION NUMBER: 07/874,491
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/827,682
; PRIOR FILING DATE: 1992-01-29
; PRIOR APPLICATION NUMBER: 07/749,568
; PRIOR FILING DATE: 1991-08-26
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T helper epitope HBC 128-140
US-08-464-496-19

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
|||||
DB 1 TPPAYRPPNAPIL 13

RESULT 3
US-08-788-822A-16
; Sequence 16, Application US/08788822A
; Patent No. 6413935
; GENERAL INFORMATION:
; APPLICANT: Alexander, Jeffrey L.
; APPLICANT: Derrees, Shawn
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Induction of Immune Response Against
; TITLE OF INVENTION: Desired Determinants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,822A
; FILING DATE: 22-JAN-1997

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
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DB 1 TPPAYRPPNAPIL 13

RESULT 4
US-08-197-484-113
; Sequence 113, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990

```

; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-113

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 5
US-09-311-784A-49
; Sequence 49, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-09-311-784A-49

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 6
US-09-664-945-50
; Sequence 50, Application US/09664945
; Patent No. 6660842
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
; FILE REFERENCE: TRIPEP.007CP3
; CURRENT APPLICATION NUMBER: US/09/664,945
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
US-09-664-945-50

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 7
PCT-US92-07218-19
; Sequence 19, Application PC/TUS9207218
; GENERAL INFORMATION:
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Chesnut, Robert W.
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; TITLE OF INVENTION: EPITOPES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US92/07218
; FILING DATE: 19920826
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-26-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

PCT-US92-07218-19

Query Match 100.0%; Score 74; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
| | | | | | | | | | | | |
DB 1 TPPAYRPPNAPIL 13

RESULT 8

PCT-US95-02121-113
; Sequence 113, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTIL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-113

Query Match 100.0%; Score 74; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
| | | | | | | | | | | | |
DB 1 TPPAYRPPNAPIL 13

RESULT 9

PCT-US95-16415-9
; Sequence 9, Application PC/TUS9516415
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute

; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
; CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16415
; FILING DATE: 13-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,558
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: 433.1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-16415-9

Query Match 100.0%; Score 74; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
| | | | | | | | | | | | |
DB 1 TPPAYRPPNAPIL 13

RESULT 10

US-09-311-784A-124
; Sequence 124, Application US/09311784A
; Patent No. 633482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 124
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBVcore128

US-09-311-784A-124

Query Match 100.0%; Score 74; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 11

US-08-737-896-7

Sequence 7, Application US/08737896
Patent No. 6168804
GENERAL INFORMATION:
APPLICANT: Samuel, John
TITLE OF INVENTION: METHOD FOR ELICITING TH1-SPECIFIC
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,896
FILING DATE: 24-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,499
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: PCT/US96/09551
FILING DATE: 07-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07254/037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Hbcag

US-08-737-896-7
Query Match 100.0%; Score 74; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 3 TPPAYRPPNAPIL 15

RESULT 12

PCT-US96-09951-7

Sequence 7, Application PC/TUS9609951
GENERAL INFORMATION:
APPLICANT: The Governors of the University of Alberta
TITLE OF INVENTION: A METHOD FOR ELICITING A TH1-SPECIFIC

TITLE OF INVENTION: IMMUNE RESPONSE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09951
FILING DATE: 06-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Learl, June M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: 07254/037W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Hbcag
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
PCT-US96-09951-7

Query Match 100.0%; Score 74; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 3 TPPAYRPPNAPIL 15

RESULT 13

US-09-100-409A-45
Sequence 45, Application US/09100409A
Patent No. 6090388
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
PREVENTION AND TREATMENT OF HIV INFECTION AND
IMMUNE DISORDERS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
#1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,409A

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; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-409A-45
Query Match 100.0%; Score 74; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 9 TPPAYRPPNAPIL 21

RESULT 14
PCT-US95-13841-13
; Sequence 13, Application PC/TUS9513841
; GENERAL INFORMATION:
; APPLICANT: United Biomedical Inc; Walfield, Alan M.;
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Synthetic Igs Membrane Anchor
; TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13841
; FILING DATE: 25-OCT-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/328,519
; FILING DATE: 25-OCT-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin, Maria C.H.
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-13841-13
Query Match 100.0%; Score 74; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-409A-45
Query Match 100.0%; Score 74; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 9 TPPAYRPPNAPIL 21

RESULT 15
US-08-464-496-20
; Sequence 20, Application US/08464496
; Patent No. 6322789
; GENERAL INFORMATION:
; APPLICANT: Epiimmune, Inc.
; APPLICANT: Vitello, Maria
; APPLICANT: Chesnut, Robert
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; TITLE OF INVENTION: EPITOPES
; FILE REFERENCE: 39963-20001.13
; CURRENT APPLICATION NUMBER: US/08/464,496
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 07/935,811
; PRIOR FILING DATE: 1992-08-26
; PRIOR APPLICATION NUMBER: 07/874,491
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/827,682
; PRIOR FILING DATE: 1992-01-29
; PRIOR APPLICATION NUMBER: 07/749,568
; PRIOR FILING DATE: 1991-08-26
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T helper epitope HBC 128-140
US-08-464-496-20
Query Match 100.0%; Score 74; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

Search completed: August 9, 2004, 13:29:48
Job time : 19 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2004, 13:23:00 ; Search time 52 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPPAYRPPNPAIL 13

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1980s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	13	2 AAR33501	Aar33501 T helper
2	74	100.0	13	2 AAR78929	Aar78929 HBC 128-1
3	74	100.0	13	2 AAW39439	Aaw39439 Mouse H-2
4	74	100.0	13	2 AAW50117	Aaw50117 Pan DR bi
5	74	100.0	13	3 AAY52556	Aay52556 HBV core
6	74	100.0	13	4 AAG64542	Aag64542 T-helper
7	74	100.0	13	4 AAE02681	Aae02681 Hepatitis
8	74	100.0	13	4 AAE00471	Aae00471 Immunogen
9	74	100.0	13	4 AAG62426	Aag62426 Hepatitis
10	74	100.0	13	4 AAB82775	Aab82775 H-2 I-Ab
11	74	100.0	13	4 AAU00614	Aau00614 Hepatitis
12	74	100.0	13	5 AAU70851	Aau70851 HBV pepti
13	74	100.0	13	5 ABB76787	Abb76787 HBV pepti
14	74	100.0	13	5 AEG62860	Aeg62860 Antigenic
15	74	100.0	13	5 ABP52344	Abp52344 TH epitop
16	74	100.0	13	5 ABP52307	Abp52307 T helper
17	74	100.0	13	5 ABP52350	Abp52350 TH epitop
18	74	100.0	13	5 ABP51503	Abp51503 T helper
19	74	100.0	13	6 ABR44095	Abp44095 HBV core
20	74	100.0	13	6 ABP98778	Abp98778 HBV core
21	74	100.0	13	6 AAO22990	Aao22990 p128-40 I
22	74	100.0	13	6 ABU63009	Abu63009 HBV core
23	74	100.0	13	7 ADC21494	Adc21494 Hepatitis
24	74	100.0	13	7 ADC85105	Adc85105 HBV assoc
25	74	100.0	13	7 ADD35647	Add35647 Hepatitis

ALIGNMENTS

RESULT 1

AAR33501
ID AAR33501 standard; peptide; 13 AA.

XX AAR33501;

XX AC

XX 25-MAR-2003 (revised)

DT 01-JUL-1993 (first entry)

XX XX

DE T helper peptide HBC 128-140.

XX XX

KW Hepatitis B virus; HBV; core antigen; MHC class I; chronic; acute;

KW infection; identification; HLA-restricted.

XX OS

OS Synthetic.

XX PN

PN W09303764-A1.

XX XX

XX 04-MAR-1993.

XX PF

PF 26-AUG-1992; 92WO-US007218.

XX XX

XX 26-AUG-1991; 91US-00749568.

PR 29-JAN-1992; 92US-00827682.

PR 27-APR-1992; 92US-00874491.

XX PA

PA (CYTE-) CYTEL CORP.

XX XX

XX Vitiello MA, Chesnut RW;

PI WPI; 1993-093728/11.

XX XX

DR Cytotoxic T-lymphocyte stimulating peptide(s) - derived from hepatitis B virus useful for treating, preventing and diagnosing infection.

XX PT

PT Disclosure; Page 21; 89pp; English.

XX PS

XX This is a T helper epitope peptide, the sequence of which is derived from hepatitis B virus (HBV) core antigen amino acids 128-140. It may be used in a conjugate with cytotoxic T-lymphocyte stimulating (CTL) peptides to enhance an individual's immunity by providing cell-mediated immunity and protective antibodies. (Updated on 25-MAR-2003 to correct FN field.)

XX XX

XX Sequence 13 AA;

SQ

Query Match 100.0%; Score 74; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 2
 AAR78929
 ID AAR78929 standard; peptide; 13 AA.
 XX AC AAR78929;
 XX DT 25-MAR-2003 (revised)
 XX DT 27-MAR-1996 (first entry)
 XX DE HBC 128-140 cytotoxic T lymphocyte epitope.
 XX KW HBC 128-140; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte;
 XX KW antigens; treatment; disease prevention; hepatitis B.
 XX OS Hepatitis B virus.
 XX PN WO9522317-A1.
 XX PD 24-AUG-1995.
 XX PF 16-FEB-1995; 95WO-US002121.
 XX PR 16-FEB-1994; 94US-00197484.
 XX PA (CYTE-) CYTEL CORP.
 XX PI Vitello MA, Chesnut RW, Sette AD, Celis E, Grey H;
 XX DR WPI; 1995-302545/39.
 XX PT Compn. inducing cytotoxic T lymphocyte response to pref. viral,
 XX PT bacterial, parasitic or tumour antigens - useful in the treatment and
 XX PT prevention of diseases associated with the antigen e.g. hepatitis B.
 XX PS Example 4; Page 52; 109pp; English.
 XX CC A compn. which induces a cytotoxic T lymphocyte (CTL) response to a
 XX CC hepatitis B virus (HBV) antigen (Ag) in a mammal comprises, a HBV CTL Ag
 XX CC response inducing peptide (i.e. AAR78929) and a lipid conjugated helper T
 XX CC cell inducing peptide. The compn. is useful in the treatment and
 XX CC prevention of hepatitis B. (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. NO. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 3
 AAW39439
 ID AAW39439 standard; peptide; 13 AA.
 XX AC AAW39439;
 XX DT 11-JUN-1998 (first entry)
 XX DE Mouse H-2 I-Ab-restricted HBV core antigen-derived T helper epitope.
 XX KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
 XX KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
 XX KW disease; anti-tumour; anti-viral.
 XX PN

OS Synthetic.
 OS Mus sp.
 XX WO9741440-A1.
 XX PD 06-NOV-1997.
 XX PF 28-APR-1997; 97WO-NL000229.
 XX PR 26-APR-1996; 96EP-00201145.
 XX PR 23-DEC-1996; 96EP-00203670.
 XX PA (UYLE-) RIJKSUNIV LEIDEN.
 XX PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
 XX PI Van Der Burg SH, Kast WM, Toes REM, Offringa R, Melief CJM;
 XX WPI; 1997-549891/50.
 XX PT Method of selecting T cell peptide epitope(s) - by measuring the
 XX PT stability of HLA class I-peptide complexes on intact B cells.
 XX PS Example 2; Page 21; 109pp; English.
 XX CC Peptides AAW39430-W39734 are used in a novel method for the selection of
 XX CC immunogenic T-cell peptide epitopes present in polypeptide antigens.
 XX CC Peptide AAW39439 is a mouse H-2 I-Ab restricted HBV core antigen-derived
 XX CC T helper epitope which is injected into HLA-A*0201Kb transgenic mice. The
 XX CC method involves the identification of peptide sequences capable of
 XX CC binding to an HLA (human leukocyte antigen) class I molecule and
 XX CC measuring the binding of this epitope peptide to the HLA class I peptide.
 XX CC The stability of binding of the peptide and MHC (major histocompatibility
 XX CC complex) class I molecule is measured on intact human B cells carrying
 XX CC the MHC molecule at their cell surfaces. The method can be used to select
 XX CC peptide epitopes for generating vaccines against a disease associated
 XX CC with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are
 XX CC especially T-cell peptide epitopes with strong anti-tumour and anti-viral
 XX CC immune responses
 XX SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. NO. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 4
 AAW50117
 ID AAW50117 standard; peptide; 13 AA.
 XX AC AAW50117;
 XX DT 30-JUN-1998 (first entry)
 XX DE Pan DR binding peptide (14).
 XX KW Pan DR binding peptide; antigen binding site; MHC molecule; DR locus.
 XX OS Synthetic.
 XX PN US5736142-A.
 XX PD 07-APR-1998.
 XX PF 14-SEP-1994; 94US-00305871.
 XX PR 14-SEP-1993; 93US-00121101.
 XX PA (CYTE-) CYTEL CORP.


```

PT HIV vaccines.
XX
PS Example 7; Page 42; 383pp; English.
XX
CC The invention relates to identification of cytotoxic T cell lymphocyte
CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
CC are a major protective mechanism against viral diseases. Antibodies may
CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
CC prevent infection of cells in the host, but CTL will limit viral
CC production by killing the cell. The CTL epitopes are useful in medicine,
CC in the manufacture of vaccines or diagnostic agents. The present sequence
CC is that of a T-helper epitope peptide useful to the invention
XX
XX Sequence 13 AA;
XX
XX Query Match 100.0%; Score 74; DB 4; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TPPAYRPPNPAPIL 13
XX | | | | | | | | | |
XX Db 1 TPPAYRPPNPAPIL 13
XX
XX RESULT 8
XX AAE00471
XX ID AAE00471 standard; peptide; 13 AA.
XX AC AAE00471;
XX DT 19-JUN-2001 (first entry)
XX DE Hepatitis B virus core (HBVc) tumour epitopic peptide.
XX KW Tumour epitope; cytostatic; immunostimulant; gene therapy;
XX middle glycoprotein; Hepatitis B virus core; cytotoxic response;
XX immune response; cytotoxic T lymphocyte; CTL; HBVc; HLA;
XX human leucocyte antigen.
XX OS Hepatitis B virus.
XX PN WO200123577-A2.
XX PD 05-APR-2001.
XX PF 29-SEP-2000; 2000WO-EP009900.
XX PR 30-SEP-1999; 99US-0156945P.
XX PA (INSP ) INST PASTEUR.
XX PI Firat H, Lemornier F, Langlade-Demoyen P, Michel M, Suhrbier AA;
XX WPI; 2001-266164/27.
XX
XX Novel polynucleotide having DNA sequence encoding tumor antigen epitope
XX inserted in part of coding sequence of middle glycoprotein of Hepatitis B
XX virus, used to induce immune response against tumor-specific antigen.
XX
XX Example 1; Page 13; 36pp; English.
XX
XX The present invention relates to an isolated or purified polynucleotide
XX containing a DNA sequence coding for at least one tumour epitope of a
XX tumour antigen inserted into part of the coding sequence of the middle
XX glycoprotein of the Hepatitis B virus (HBV). The polynucleotide is useful
XX for optionally evaluating cytotoxic responses in the individual's
XX lymphocyte population. It induces an immune response against at least one
XX tumour specific antigen or tissue specific antigen. The vector comprising
XX the polynucleotide induces in vivo, cellular and/or humoral immune
XX response. The composition comprising the polynucleotide induces in vivo,
XX cytotoxic T lymphocyte (CTL) against one or more antigens or epitopes
XX present on the hybrid protein. The polynucleotide is also useful in gene
XX therapy. The present sequence is a Hepatitis B virus core (HBVc) tumour
XX epitopic peptide. This peptide elicits HLA (human leucocyte antigen)-A2.1
XX - restricted CTL response in mice
XX
XX Sequence 13 AA;
XX
XX Query Match 100.0%; Score 74; DB 4; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TPPAYRPPNPAPIL 13
XX | | | | | | | | | |
XX Db 1 TPPAYRPPNPAPIL 13
XX
XX RESULT 7
XX AAE02681
XX ID AAE02681 standard; peptide; 13 AA.
XX AC AAE02681;
XX DT 06-AUG-2001 (first entry)
XX DE Hepatitis B virus HBVc helper peptide.
XX KW Cytostatic; antibacterial; antifungal; gene therapy; vaccine; antiviral;
XX tumour; epitope; glycoprotein; hepatitis B virus; HBV; immune response;
XX CTL; cytotoxic T lymphocyte; HLA; human leucocyte antigen.
XX OS Hepatitis B virus.
XX PN WO200127291-A1.
XX PD 19-APR-2001.
XX PF 29-SEP-2000; 2000WO-EP009902.
XX PR 12-OCT-1999; 99US-0158356P.
XX PA (INSP ) INST PASTEUR.
XX PI Firat H, Lemornier F, Langlade-Demoyen P;
XX WPI; 2001-282038/29.
XX
XX New polynucleotide comprising at least one viral, fungal, bacterial, or
XX tumor epitope of an antigen, capable of inducing a cellular response.
XX
XX Example 1; Page 23; 70pp; English.
XX
XX The invention relates to polynucleotide containing at least a part of the
XX coding sequence of the middle glycoprotein of hepatitis B virus (HBV) in
XX which is inserted a DNA sequence coding for an epitope comprising at
XX least one viral, fungal, bacterial, or tumour epitope of an antigen,
XX capable of inducing a cellular response. Nucleic acids and compositions
XX of the invention are useful for inducing in vivo a CTL (cytotoxic T
XX lymphocyte) response against several epitopes of one or more, bacterial,
XX viral, fungal, or tumour antigens. A composition of the invention
XX produces an immune response against HIV antigen and are used in the
XX production of vaccines. The polynucleotides of the invention are also
XX used in gene therapy. The present sequence is hepatitis B virus helper
XX peptide. This peptide is co-injected with human epitopes in order to
XX elicit HLA (human leucocyte antigen) -A2.1-restricted CTL response in
XX mice

```

XX Hepatitis B core antigen peptide.
 XX
 XX Telomerase reverse transcriptase; hTERT; human; cytotoxic T lymphocyte;
 KW major histocompatibility complex; cancer; tumour;
 KW human leucocyte antigen; HLA-A2.1; HBVC; vaccine.
 XX
 XX Hepatitis B virus.
 OS
 XX WO200160391-A1.
 PN
 XX 23-AUG-2001.
 PD
 XX 15-FEB-2001; 2001WO-US005143.
 XX
 XX 15-FEB-2000; 2000US-0182685P.
 PR
 XX 15-FEB-2001; 2001US-00182685.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Zanetti M;
 PI
 XX WPI; 2001-536552/59.
 DR
 XX Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,
 PT for treating cancers or tumors or for inducing immune response against
 PT tumors, comprises a telomerase reverse transcriptase peptide.
 XX
 XX Example 1; Page 12; 52pp; English.
 PS
 XX
 XX The present sequence is that of a hepatitis B virus core antigen (HBVc)
 CC peptide comprising amino acid residues 128-140. The peptide was used to
 CC immunise HHD mice and results were compared with those obtained using
 CC human telomerase reverse transcriptase (hTERT) HLA-A2.1+ restricted
 CC peptide p540 (see AAB82772). The induction of CTL responses in vitro and
 CC in vivo, and the susceptibility to lysis of tumour cells of various
 CC origins by hTERT CTL suggest that hTERT could serve as a universal cancer
 CC vaccine for humans. A claimed universal vaccine for treating tumours of
 CC any origin comprises at least 1 hTERT peptide. The peptide is 7-15 amino
 CC acid residues in length and may be modified to enhance binding to the
 CC major histocompatibility complex. Also claimed is a method for inducing
 CC and enhancing a CTL response against cancer cells, involving harvesting
 CC blood leucocytes, pulsing with hTERT, and contacting cancer cells with the
 CC claimed leucocytes. A method for targeting CTL to tumour cells is also
 CC claimed, and involves administering a hTERT peptide to a mammal,
 CC especially a cancer patient. (Updated on 06-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13
 RESULT 11
 AAU00614
 ID AAU00614 standard; peptide; 13 AA.
 XX
 AC AAU00614;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE H-2 I-AB-restricted HBV core antigen-derived T helper epitope.
 XX
 XX Human; MUC1; antigenic peptide; major histocompatibility complex; MHC-I;
 KW glycoprotein; cytotoxic T lymphocytes; T cell response; cancer; vaccine;
 KW cancer gene therapy; diagnosis; treatment; inflammatory disorder; HBV;
 KW organ transplant rejection; graft versus host disease.

RESULT 9
 AAG62426
 ID AAG62426 standard; peptide; 13 AA.
 XX
 AC AAG62426;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Immunogenic peptide HBV core SEQ ID 30.
 XX
 XX Class I epitope; immunogenic; heteroclitic analogue; immune response;
 KW antigen display; viral disease; cancer.
 XX
 OS Synthetic.
 XX
 XX WO200136452-A2.
 PN
 XX 25-MAY-2001.
 PD
 XX 20-NOV-2000; 2000WO-US031856.
 PF
 XX 18-NOV-1999; 99US-0166529P.
 PR
 XX 06-OCT-2000; 2000US-0239008P.
 PR
 XX (EPTM-) EPIMMUNE INC.
 PA
 XX Tangri S, Sette A, Ishioka G;
 PI
 XX WPI; 2001-355609/37.
 DR
 XX Enhancing immunogenicity of peptide containing class I epitope, useful
 PT for treating cancer, comprises providing (semi-)conservative amino acid
 PT substitutions at specified positions of these epitopes.
 XX
 XX Disclosure; Fig 1A; 96pp; English.
 PS
 XX This invention relates to a method of enhancing the immunogenicity of a
 CC peptide, where the peptide contains a class I epitope. The invention
 CC includes methods for preparing peptides containing epitopes which have
 CC enhanced ability to effect an immune response (compared to wild-type
 CC epitopes). The peptides are referred to as heteroclitic analogues. The
 CC method is useful for eliciting an immune response by contacting CTLs with
 CC the immunogenically enhanced peptide in vitro in the presence of an
 CC antigen presenting cell, or by administering to a subject a nucleic acid
 CC molecule comprising a nucleotide sequence encoding the peptide. The
 CC peptides are useful as reagents to evaluate an immune response and the
 CC efficacy of the vaccine, and for making antibodies. The heteroclitic
 CC analogues are useful in immunological compositions for the treatment of
 CC viral diseases, cancer, and other conditions which are characterised by
 CC displayed antigens on target cells. The present sequence represents a
 CC class I epitope which may be used in the method of the invention
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13
 RESULT 10
 AAB82775
 ID AAB82775 standard; protein; 13 AA.
 XX
 AC AAB82775;
 XX
 XX 06-AUG-2003 (revised)
 DT 29-OCT-2001 (first entry)
 DT

XX Hepatitis B virus.
 OS WO200118035-A2.
 PN
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2006WO-EP008761.
 XX
 PR 08-SEP-1999; 95GB-00021242.
 PR 10-SEP-1999; 99EP-00402237.
 PR 03-MAR-2000; 2000US-0187215P.
 XX
 PA (TRGE) TRANSGENE SA.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX
 PI Taylor-Papadimitriou J, Heukamp LC, Offringa R, Melief CJM;
 PI Acres B, Thomas M;
 XX
 DR WPI; 2001-235187/24.
 XX
 PT New antigenic polypeptides of MUC-1 protein which activate cytotoxic T
 PT lymphocyte proteins and their analogs, useful for identifying a major
 PT histocompatibility complex class I restricted T cell response and for
 PT diagnosing cancer.
 XX
 PS Example 5; Page 42; 81pp; English.
 XX
 CC The sequence represents an H-2 I-Ab-restricted hepatitis B virus (HBV)
 CC core antigen-derived T helper epitope used in testing of human MUC1
 CC polypeptide derivatives through a cytotoxic T lymphocyte (CTL) assay.
 CC Derivative antigenic peptides of MUC1 protein bind at least one major
 CC histocompatibility complex class I (MHC-I) glycoprotein, which activates
 CC cytotoxic T lymphocytes to induce a protective response against tumours.
 CC Diagnosis of cancer involves determining the presence or absence in a
 CC host cell of MHC class I restricted T cell response to a MUC1 derivative,
 CC where the presence of the MHC class I restricted T cell response
 CC indicates that the host has cancer. Measurement of the level of MHC class
 CC I restricted T cell response is also useful to monitor the severity of
 CC cancer, a larger response indicating a more severe cancer. MUC1
 CC derivatives are useful in cancer therapy and to follow MUC1 specific
 CC immune responses in patients during the course of disease and/or
 CC treatment. MUC1 DNA is useful in cancer gene therapy, vaccination and
 CC diagnosis. Compositions of the sequences are used in vaccines and
 CC treatments against cancer or diseases caused by an immune response, such
 CC as an inflammatory disorder, organ transplant rejection or graft versus
 CC host disease
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNPAPIL 13
 DB 1 TPPAYRPPNPAPIL 13
 RESULT 12
 AAU70851
 ID AAU70851 standard; peptide; 13 AA.
 XX
 AC AAU70851;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Hepatitis B virus antigen binding partner #83.
 XX
 KW Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;
 KW antiinflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg;
 KW B cell mediated processing; T cell proliferation; cytokine production;
 KW immune system response.

XX Synthetic.
 OS WO200181421-A2.
 PN
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-IB000844.
 XX
 PR 21-APR-2000; 2000US-00556605.
 XX
 PA (TRIP-) TRIPEP AB.
 XX
 PI Sallberg M;
 XX
 DR WPI; 2002-055347/07.
 XX
 PT Novel peptide that binds to hepatitis B virus core or E antigen, useful
 PT for treating and preventing hepatitis B virus infection.
 XX
 PS Example 6; Page 28; 82pp; English.
 XX
 CC The invention relates to an isolated or purified peptide (I) which binds
 CC Hepatitis B virus (HBV) core antigen (HbcAg) or HBV E antigen (HBeAg).
 CC (I) is useful for treating or preventing Hepatitis B virus (HBV)
 CC infection, by identifying a subject in need of a molecule that inhibits
 CC HBV infection, and providing the subject with (I). (I) is also useful for
 CC determining the presence of HBV in a biological sample, and for
 CC inhibiting B cell mediated processing and uptake of HbcAg and/or HBeAg,
 CC by determining whether (I) inhibits B cell mediated processing and uptake
 CC of HbcAg and/or HBeAg by performing an assay of T cell proliferation or
 CC cytokine production. (I) is also useful for modulating an immune system
 CC response. (I) is useful as a template for a design of synthetic molecules
 CC including peptides, derivatives or modified peptides, peptidomimetics and
 CC chemicals. (I) is also useful as biotechnological tool, diagnostic
 CC reagent and as active ingredient in pharmaceuticals. (I) is also useful
 CC as detection reagents in conventional immunochemical techniques, as
 CC diagnostic reagents to detect HBV in biological sample, and to determine
 CC the efficacy of an HBV treatment protocol by monitoring the levels of
 CC HbcAg and/or HBeAg during and after treatment. AAU70766-AAU70876
 CC represent Hepatitis B virus (HBV) core antigen (HbcAg) or HBV E antigen
 CC (HBeAg) binding partners as described in the invention
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNPAPIL 13
 DB 1 TPPAYRPPNPAPIL 13
 RESULT 13
 ABB76787
 ID ABB76787 standard; peptide; 13 AA.
 XX
 AC ABB76787;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE HBV peptide 128-140.
 XX
 KW Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;
 KW human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.
 XX
 OS Unidentified.
 XX
 PN FR2812087-A1.
 XX
 PD 25-JAN-2002.
 XX

PF 21-JUL-2000; 2000FR-00009591.
 XX
 PR 21-JUL-2000; 2000FR-00009591.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Kosmatopoulos K, Tourdot S, Scardino A, Gross DA;
 XX
 DR WPI; 2002-189846/25.
 XX
 XX Identifying subdominant or cryptic epitopes, useful in immunotherapy of
 PT cancer and viral infection, comprises testing modified, non-immunogenic
 PT peptides for induction of cytotoxic T cells.
 XX
 PS Example 1; Page 14; 62pp; French.
 XX
 CC The present invention relates to subdominant/cryptic epitopes that are
 CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The
 CC epitopes or chimeric polypeptides containing them and nucleic acid
 CC encoding them are useful for preventative or curative immunotherapy of
 CC cancer and viral infections, particularly where used as vaccines. The
 CC present peptide was used to illustrate the invention
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TPPAYRPPNAPIL 13
 Db 1 TPPAYRPPNAPIL 13
 RESULT 14
 ID ABG62860 standard; peptide; 13 AA.
 XX
 AC ABG62860;
 XX
 DT 21-AUG-2002 (first entry)
 XX
 DE Antigenic domain peptide from a Hepatitis B virus protein.
 XX
 KW Ligand/receptor specificity exchanger; antibody; pathogen receptor;
 KW bacterial infection; viral infection; yeast infection; cancer;
 KW parasitic infection; fungal infection; proliferation; antibacterial;
 KW virucide; cytostatic; antifungal; antigenic domain.
 XX
 OS Hepatitis B virus.
 XX
 FN WO200224887-A2.
 XX
 PD 28-MAR-2002.
 XX
 XX 19-SEP-2001; 2001WO-IB002327.
 PF
 XX 19-SEP-2000; 2000US-00664025.
 PR
 XX (TRIP-) TRIPEP AB.
 PA
 XX Sallberg M, Flock J;
 PI
 XX WPI; 2002-499707/52.
 DR
 XX Novel ligand/receptor specificity exchanger that redirects antibodies to
 PT receptors on pathogen or tumor cell, has specificity domain having ligand
 PT for receptor, and antigenic domain having epitope of pathogen or toxin.
 XX
 XX Claim 14; Page 14; 79pp; English.
 PS
 XX The present invention relates to ligand/receptor specificity exchangers
 CC comprising at least one specificity domain comprising a ligand for a

CC receptor, and at least one antigenic domain joined to the specificity
 CC domain, where the antigenic domain comprises an epitope of a pathogen or
 CC toxin. The ligand/receptor specificity exchangers redirect antibodies to
 CC receptors present on pathogens. They are useful for preventing and
 CC treating human diseases such as bacterial, viral, yeast, parasitic and
 CC fungal infections, and cancer. These compositions act by inhibiting
 CC proliferation of pathogens, or cancer cells. One of the prophylactic
 CC applications of the ligand/receptor specificity exchangers includes
 CC coating or crosslinking it to a medical device or implant which include
 CC implantable medical devices that tend to serve as foci for infection by a
 CC number of bacterial species. ABG62853-ABG62869 represent antigenic domain
 CC peptides used in the methods of the present invention
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TPPAYRPPNAPIL 13
 Db 1 TPPAYRPPNAPIL 13
 RESULT 15
 ID ABP52344 standard; peptide; 13 AA.
 XX
 AC ABP52344;
 XX
 DT 17-OCT-2002 (first entry)
 XX
 DE TH epitope.
 XX
 KW Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;
 KW tumour; immune response; cancer; vaccine; antibody.
 XX
 OS Synthetic.
 XX
 FN WO200258728-A2.
 XX
 PD 01-AUG-2002.
 XX
 XX 28-JAN-2002; 2002WO-GB000354.
 PF
 XX 26-JAN-2001; 2001GB-00002145.
 PR
 XX (SCAN-) SCANCEL LTD.
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 XX Durrant LG, Parsons T, Robins A;
 PI
 XX WPI; 2002-608418/65.
 DR
 XX Use of polypeptides and nucleic acids encoding the polypeptides, in
 PT manufacturing medicament for stimulating a cytotoxic T cell response and
 PT for preventing or treating cancer, e.g. colorectal, lung, breast or
 PT ovarian cancer.
 XX
 XX Example 11; Page 45; 87pp; English.
 PS
 XX The present invention describes the use of a polypeptide (I) in the
 CC manufacture of a medicament for stimulating a cytotoxic T cell response,
 CC where (I) comprises a first portion comprising the part of human Fc that
 CC binds to CD64 and a second portion comprising one or more heterologous T
 CC cell epitopes. Also described is a method of stimulating a cytotoxic T
 CC cell response in a patient such as a mammal, preferably human, by
 CC administering (I) to the patient. (I) has cytostatic activity and can be
 CC used in vaccine production. (I) and the nucleic acid encoding (I) are
 CC useful in the manufacture of a medicament for stimulating cytotoxic T
 CC cell response. The medicament is useful for preventing and/or treating
 CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The
 CC medicament stimulates cytotoxic and helper T cell responses. The

CC antibodies are useful as vaccines to stimulate helper and cytotoxic T
CC cell responses. The polypeptides and nucleic acids are useful in
CC optimising immunisation schedules for enhancing a protective immune
CC response against cancer. The present sequence represents a TH epitope
CC which is used in an example from the present invention

xx

SQ Sequence 13 AA;

Query Match . 100.0%; Score 74; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 1 TPPAYRPPNAPIL 13

Search completed: August 9, 2004, 13:27:41
Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2004, 13:28:56 ; Search time 43 Seconds
(without alignments)
94.834 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74
Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 31362936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	13	9	US-09-839-447A-86
2	74	100.0	13	10	US-09-277-074-9
3	74	100.0	13	12	US-09-277-064-9
4	74	100.0	13	12	US-10-371-525-49
5	74	100.0	13	12	US-10-372-735-55
6	74	100.0	13	12	US-10-182-252A-1374
7	74	100.0	13	12	US-10-333-430-63
8	74	100.0	13	12	US-09-788-110A-4
9	74	100.0	13	12	US-09-055-744-10
10	74	100.0	13	13	US-10-106-487-22
11	74	100.0	13	14	US-10-128-711-113
12	74	100.0	13	14	US-10-116-118-30
13	74	100.0	13	15	US-10-371-069-49
14	74	100.0	13	15	US-10-371-645-49
15	74	100.0	13	15	US-10-371-260-49

16	74	100.0	13	15	US-10-369-060A-86
17	74	100.0	13	15	US-10-388-337-22
18	74	100.0	13	15	US-10-608-541-50
19	74	100.0	14	12	US-10-371-525-124
20	74	100.0	14	15	US-10-371-069-124
21	74	100.0	14	15	US-10-371-645-124
22	74	100.0	14	15	US-10-371-260-124
23	74	100.0	16	14	US-10-106-876-3
24	74	100.0	18	14	US-10-106-876-10
25	74	100.0	20	9	US-09-839-447A-107
26	74	100.0	20	15	US-10-369-060A-107
27	74	100.0	21	8	US-08-785-997-43
28	74	100.0	21	10	US-09-387-340-43
29	74	100.0	21	10	US-09-386-591-43
30	74	100.0	23	14	US-10-128-711-114
31	74	100.0	26	14	US-10-128-711-115
32	74	100.0	80	12	US-10-371-525-22
33	74	100.0	80	15	US-10-371-069-22
34	74	100.0	80	15	US-10-371-645-22
35	74	100.0	80	15	US-10-371-260-22
36	74	100.0	118	12	US-10-371-525-8
37	74	100.0	118	15	US-10-371-069-8
38	74	100.0	118	15	US-10-371-645-8
39	74	100.0	118	15	US-10-371-260-8
40	74	100.0	119	12	US-10-371-525-10
41	74	100.0	119	15	US-10-371-069-10
42	74	100.0	119	15	US-10-371-645-10
43	74	100.0	119	15	US-10-371-260-10
44	74	100.0	136	12	US-10-371-525-12
45	74	100.0	136	15	US-10-371-069-12

ALIGNMENTS

RESULT 1
US-09-839-447A-86
; Sequence 86, Application US/09839447A
; Patent No. US20020058247A1
; GENERAL INFORMATION:
; APPLICANT: Sallberg, Matti
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; FILE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
; FILE REFERENCE: TRIPEP 020CPI
; CURRENT APPLICATION NUMBER: US/09/839,447A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/556605
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-839-447A-86

Query Match 100.0%; Score 74; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
|||||
DB 1 TPPAYRPPNAPIL 13

RESULT 2
US-09-277-074-9
; Sequence 9, Application US/09277074
; Publication No. US2003002820A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Linda A.

```
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR2155S
; CURRENT APPLICATION NUMBER: US/09/277,074
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-277-074-9

Query Match      100.0%; Score 74; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 3
US-09-277-064-9
; Sequence 9, Application US/09277064
; Publication No. US20030064916A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR2152S
; CURRENT APPLICATION NUMBER: US/09/277,064
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-277-064-9

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 4
US-10-371-525-49
; Sequence 49, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
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; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-525-49

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 5
US-10-372-735-55
; Sequence 55, Application US/10372735
; Publication No. US20030225251A1
; GENERAL INFORMATION:
; APPLICANT: Saliberg, Mattci
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; FILE REFERENCE: TRIPEP.7AUC4CP1
; CURRENT APPLICATION NUMBER: US/10/372,735
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/234,579
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-06
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE95/00468
; PRIOR FILING DATE: 1995-04-27
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/664,025
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: PCT/IB01/02327
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 10/153,271
; PRIOR FILING DATE: 2002-05-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptides
US-10-372-735-55

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13
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RESULT 6
 US-10-182-252A-1374
 ; Sequence 1374, Application US/10182252A
 ; Publication No. US20040072162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FOMSGAARD, ANDERS
 ; APPLICANT: BRUNAK, SOREN
 ; APPLICANT: BUUS, SOREN
 ; APPLICANT: CORBET, SYLVIE
 ; APPLICANT: LAUEMOLLER, SANNE LISE
 ; APPLICANT: HANSEN, JAN
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
 ; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
 ; FILE REFERENCE: 030307/0205
 ; CURRENT APPLICATION NUMBER: US/10/182,252A
 ; CURRENT FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059
 ; PRIOR FILING DATE: 2001-01-29
 ; PRIOR APPLICATION NUMBER: EP 00610017.6
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/179,333
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 1388
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1374
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-182-252A-1374

Query Match 100.0%; Score 74; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 7
 US-10-333-430-63
 ; Sequence 63, Application US/10333430
 ; Publication No. US20040072240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INSERM
 ; APPLICANT: INSTITUT GUSTAVE ROUSSY
 ; APPLICANT: KOSMATOPOULOS, Kostas
 ; APPLICANT: TOURDOR, Sophie
 ; APPLICANT: SCARDINO, Antonio
 ; APPLICANT: GROSS, David, Alexandre
 ; TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
 ; TITLE OF INVENTION: IMMUNOTHERAPY
 ; FILE REFERENCE: 33339/259034
 ; CURRENT APPLICATION NUMBER: US/10/333,430
 ; CURRENT FILING DATE: 2003-10-02
 ; PRIOR APPLICATION NUMBER: FR 0009591
 ; PRIOR FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 63
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 US-10-333-430-63

Query Match 100.0%; Score 74; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 TPPAYRPPNAPIL 13

DB 1 TPPAYRPPNAPIL 13
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 US-09-788-110A-4
 ; Sequence 4, Application US/09788110A
 ; Publication No. US20040086518A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zanetti, Maurizio
 ; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
 ; TITLE OF INVENTION: Telomerase Reverse Transcriptase
 ; FILE REFERENCE: UCSD-07017
 ; CURRENT APPLICATION NUMBER: US/09/788,110A
 ; CURRENT FILING DATE: 2001-02-15
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-788-110A-4

Query Match 100.0%; Score 74; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 9
 US-09-055-744-10
 ; Sequence 10, Application US/09055744
 ; Publication No. US20010019714A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sia, Charles
 ; APPLICANT: Chong, Pele
 ; APPLICANT: Klein, Michel
 ; TITLE OF INVENTION: HIV-SPECIFIC CYTOTOXIC T-CELL RESPONSES
 ; FILE REFERENCE: 1038-746
 ; CURRENT APPLICATION NUMBER: US/09/055,744
 ; CURRENT FILING DATE: 1998-04-07
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-09-055-744-10

Query Match 100.0%; Score 74; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 10
 US-10-106-487-22
 ; Sequence 22, Application US/10106487
 ; Publication No. US20020164721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FIRAT, HUSEYIN
 ; APPLICANT: LEMONNIER, FRANCOIS
 ; APPLICANT: LANGLADE-DEMOYEN, PIERRE
 ; APPLICANT: MICHEL, MARIE-LOUISE
 ; TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION
 ; TITLE OF INVENTION: OF
 ; TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING

;/ TITLE OF INVENTION: HHD MICE
;/ FILE REFERENCE: 03495.0196 SEQUENCE LISTING
;/ CURRENT APPLICATION NUMBER: US/10/106,487
;/ CURRENT FILING DATE: 2002-03-27
;/ PRIOR APPLICATION NUMBER: 09/675,673
;/ PRIOR FILING DATE: 2000-09-29
;/ PRIOR APPLICATION NUMBER: 60/158,356
;/ PRIOR FILING DATE: 1999-10-12
;/ NUMBER OF SEQ ID NOS: 41
;/ SOFTWARE: PatentIn Ver. 2.1
;/ SEQ ID NO 22
;/ LENGTH: 13
;/ TYPE: PRI
;/ ORGANISM: Hepatitis B virus
US-10-106-487-22

Query Match 100.0%; Score 74; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 11
US-10-128-711-113
;/ Sequence 113, Application US/10128711
;/ Publication No. US20030099634A1
;/ GENERAL INFORMATION:
;/ APPLICANT: VITIELLO, Maria A.
;/ CHESTNUT, Robert W.
;/ SETTE, Alessandro D.
;/ CELIS, Esteban
;/ GRAY, Howard
;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL IMMUNITY
;/ NUMBER OF SEQUENCES: 153
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend Khourie and Crew
;/ STREET: Stuart Street Tower, One Market Plaza
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: US
;/ ZIP: 94105-1493
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/10/128,711
;/ FILING DATE: 22-Apr-2002
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/197,484
;/ FILING DATE: 16-FEB-1994
;/ APPLICATION NUMBER: US 07/935,811
;/ FILING DATE: 26-AUG-1992
;/ APPLICATION NUMBER: US 07/874,491
;/ FILING DATE: 27-APR-1992
;/ APPLICATION NUMBER: US 07/827,682
;/ FILING DATE: 29-JAN-1992
;/ APPLICATION NUMBER: US 07/749,568
;/ FILING DATE: 26-AUG-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Parmelee, Steven W.
;/ REGISTRATION NUMBER: 31,990
;/ REFERENCE/DOCKET NUMBER: 14137-26-4
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (206) 467-9600
;/ TELEFAX: (206) 623-6793
;/ INFORMATION FOR SEQ ID NO: 113:

;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 13 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: unknown
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: peptide
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-128-711-113

Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 12
US-10-116-118-30
;/ Sequence 30, Application US/10116118
;/ Publication No. US20030143672A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Tangri, Shabnam
;/ APPLICANT: Sette, Alessandro
;/ APPLICANT: Ishioka, Glenn
;/ APPLICANT: Fikes, John D.
;/ TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
;/ FILE REFERENCE: 2060.0090003
;/ CURRENT APPLICATION NUMBER: US/10/116,118
;/ CURRENT FILING DATE: 2002-08-07
;/ PRIOR APPLICATION NUMBER: US 60/166,529
;/ PRIOR FILING DATE: 1999-11-18
;/ PRIOR APPLICATION NUMBER: US 60/239,008
;/ PRIOR FILING DATE: 2000-10-06
;/ NUMBER OF SEQ ID NOS: 53
;/ SOFTWARE: PatentIn version 3.1
;/ SEQ ID NO 30
;/ LENGTH: 13
;/ TYPE: PRI
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: (HBV core)
US-10-116-118-30

Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 13
US-10-371-069-49
;/ Sequence 49, Application US/10371069
;/ Publication No. US20030216342A1
;/ GENERAL INFORMATION:
;/ APPLICANT: EPIMMUNE Inc.
;/ APPLICANT: Fikes, John D.
;/ APPLICANT: Hermanson, Gary G.
;/ APPLICANT: Sette, Alessandro
;/ APPLICANT: Ishioka, Glenn Y.
;/ APPLICANT: Livingston, Brian
;/ APPLICANT: Chesnut, Robert W.
;/ APPLICANT: Epimmune Inc.
;/ TITLE OF INVENTION: Expression Vectors for Stimulating an
;/ FILE REFERENCE: Immune Response and Methods of Using the Same
;/ FILE REFERENCE: 39963-20022.10
;/ CURRENT APPLICATION NUMBER: US/10/371,069
;/ CURRENT FILING DATE: 2003-02-21
;/ PRIOR APPLICATION NUMBER: US 09/078,904

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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-069-49
```

```
Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13
|||||
```

```
RESULT 14
US-10-371-645-49
; Sequence 49, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-645-49
```

```
Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13
|||||
```

```
RESULT 15
US-10-371-260-49
; Sequence 49, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
```

```
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-260-49
```

```
Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13
|||||
```

```
Search completed: August 9, 2004, 13:34:25
Job time : 44 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2004, 13:27:25 ; Search time 16 Seconds

(without alignments)
78.156 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	74	100.0	183	1 NKVLA2	core antigen - hep
2	74	100.0	183	1 NKVLCF	core antigen - hep
3	74	100.0	183	2 S53214	core antigen - hep
4	74	100.0	183	2 S53221	core antigen - hep
5	74	100.0	183	2 S53232	core antigen - hep
6	74	100.0	183	2 S53247	core antigen - hep
7	74	100.0	183	2 S53260	core antigen - hep
8	74	100.0	183	2 S53270	core antigen - hep
9	74	100.0	183	2 S53129	core antigen - hep
10	74	100.0	183	2 S53140	core antigen - hep
11	74	100.0	183	2 S53152	core antigen - hep
12	74	100.0	183	2 S53166	core antigen - hep
13	74	100.0	183	2 S53169	core antigen - hep
14	74	100.0	183	2 S53172	core antigen - hep
15	74	100.0	183	2 S53175	core antigen - hep
16	74	100.0	183	2 S53186	core antigen - hep
17	74	100.0	183	2 S53189	core antigen - hep
18	74	100.0	183	2 S53194	core antigen - hep
19	74	100.0	183	2 S53199	core antigen - hep
20	74	100.0	183	2 S53255	core antigen - hep
21	74	100.0	184	2 S53146	core antigen - hep
22	74	100.0	195	1 NKVLH3	core antigen - hep
23	74	100.0	211	1 NKVLA1	e antigen precursor
24	74	100.0	212	1 NKVLAH	e antigen precursor
25	74	100.0	212	1 NKVLA4	e antigen precursor
26	74	100.0	212	1 NKVLA4	e antigen precursor
27	74	100.0	212	1 NKVLJ1	e antigen precursor
28	74	100.0	212	1 NKVLJ2	e antigen precursor
29	74	100.0	212	2 S53211	e antigen precursor

30	74	100.0	212	2 S53216	e antigen precursor
31	74	100.0	212	2 S53223	e antigen precursor
32	74	100.0	212	2 S53225	e antigen precursor
33	74	100.0	212	2 S53229	e antigen precursor
34	74	100.0	212	2 S53236	e antigen precursor
35	74	100.0	212	2 S53238	e antigen precursor
36	74	100.0	212	2 S53240	e antigen precursor
37	74	100.0	212	2 S53242	e antigen precursor
38	74	100.0	212	2 S53251	e antigen precursor
39	74	100.0	212	2 S53253	e antigen precursor
40	74	100.0	212	2 S53255	e antigen precursor
41	74	100.0	212	2 S53257	e antigen precursor
42	74	100.0	212	2 S53272	e antigen precursor
43	74	100.0	212	2 S53274	e antigen precursor
44	74	100.0	212	2 S53279	e antigen precursor
45	74	100.0	212	2 S53281	e antigen precursor

ALIGNMENTS

RESULT 1

NKVLA2

core antigen - hepatitis B virus (subtype adyw)

C/Species: hepatitis B virus, HBV

A/Variety: subtype adyw

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999

C/Accession: B93217; A03711

R/Pasek, M.; Goto, T.; Gilbert, W.; Zink, B.; Schaller, H.; MacKay, P.; Leadbetter, G.;

Nature 282, 575-579, 1979

A/Title: Hepatitis B virus genes and their expression in E. coli.

A/Reference number: A93217; MUID:81012115; PMID:399329

A/Accession: B93217

A/Molecule type: DNA

A/Residues: 1-183 <PAS>

A/Cross-references: GB:J02202; NID:G329637; PIDN:AAA45486.1; PID:G329638

A/Experimental source: subtype adyw

A/Note: due to a stop codon between the alternative initiators the e antigen precursor c

C/Genetics:

A/Gene: C

C/Superfamily: hepatitis B virus core antigen

C/Keywords: core protein

F/1-183/Product: core antigen #status predicted <MAT>

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13

Db 128 TPPAYRPPNAPIL 140

RESULT 2

NKVLCF

core antigen - hepatitis B virus (strain LSH, chimpanzee)

N/Alternate names: H3C antigen

C/Species: hepatitis B virus, HBV

A/Variety: strain LSH, chimpanzee

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000

C/Accession: A28885

R/Vaudin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.

J. Gen. Virol. 69, 1383-1389, 1988

A/Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated f

A/Reference number: A92796; MUID:88258473; PMID:2838576

A/Accession: A28885

A/Molecule type: DNA

A/Residues: 1-183 <VAU>

A/Cross-references: EMBL:D00220; NID:G221505; PIDN:BAA00157.1; PID:G221506

A/Experimental source: strain LSH, chimpanzee

A/Note: due to a stop codon between the alternative initiators the e antigen precursor c

C/Genetics:

A/Gene: C

A;Variety: isolate patient Mannoni-3'94
 C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C;Accession: S53260
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A;Reference number: S53112
 A;Accession: S53260
 A;Molecule type: DNA
 A;Residues: 1-183 <LAI>
 A;Cross-references: EMBL:X85311; NID:g736187; PIDN:CAA59655.1; PID:g736190
 A;Experimental source: isolate patient Mannoni-3'94
 A;Note: due to a stop codon between the alternative initiators the e antigen precursor
 C;Genetics:
 A;Gene: C
 C;Superfamily: hepatitis B virus core antigen
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 |||||
 DB 128 TPPAYRPPNAPIL 140

RESULT 8
 S53270
 core antigen - hepatitis B virus (isolate patient Licheri-2'87)
 N;Alternate names: HBC antigen
 N;Contains: core antigen
 C;Species: hepatitis B virus, HBV
 A;Variety: isolate patient Licheri-2'87
 C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C;Accession: S53270
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A;Reference number: S53112
 A;Accession: S53270
 A;Molecule type: DNA
 A;Residues: 1-183 <LAI>
 A;Cross-references: EMBL:X85314; NID:g736201; PIDN:CAA59662.1; PID:g736204
 A;Experimental source: isolate patient Licheri-2'87
 A;Note: due to a stop codon between the alternative initiators the e antigen precursor
 C;Genetics:
 A;Gene: C
 C;Superfamily: hepatitis B virus core antigen
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 |||||
 DB 128 TPPAYRPPNAPIL 140

RESULT 9
 S53129
 core antigen - hepatitis B virus
 N;Alternate names: HBC antigen
 N;Contains: core antigen
 C;Species: hepatitis B virus, HBV
 C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C;Accession: S53129
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A;Reference number: S53112
 A;Accession: S53129
 A;Molecule type: DNA
 A;Residues: 1-183 <LAI>
 A;Cross-references: EMBL:X85254; NID:g736003; PIDN:CAA59512.1; PID:g736006

C;Genetics:
 A;Gene: C
 C;Superfamily: hepatitis B virus core antigen
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 |||||
 DB 128 TPPAYRPPNAPIL 140

RESULT 10
 S53140
 core antigen - hepatitis B virus (isolate patient Fraillis'92)
 N;Alternate names: HBC antigen
 N;Contains: core antigen
 C;Species: hepatitis B virus, HBV
 A;Variety: isolate patient Fraillis'92
 C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C;Accession: S53140
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A;Reference number: S53112
 A;Accession: S53140
 A;Molecule type: DNA
 A;Residues: 1-183 <LAI>
 A;Cross-references: EMBL:X85265; NID:g736017; PIDN:CAA59544.1; PID:g736020
 A;Experimental source: isolate patient Fraillis'92
 A;Note: due to a stop codon between the alternative initiators the e antigen precursor
 C;Genetics:
 A;Gene: C
 C;Superfamily: hepatitis B virus core antigen
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 |||||
 DB 128 TPPAYRPPNAPIL 140

RESULT 11
 S53152
 core antigen - hepatitis B virus (isolate patient Tufariello'89)
 N;Alternate names: HBC antigen
 N;Contains: core antigen
 C;Species: hepatitis B virus, HBV
 A;Variety: isolate patient Tufariello'89
 C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C;Accession: S53152
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A;Reference number: S53112
 A;Accession: S53152
 A;Molecule type: DNA
 A;Residues: 1-183 <LAI>
 A;Cross-references: EMBL:X85269; NID:g736033; PIDN:CAA59556.1; PID:g736036
 A;Experimental source: isolate patient Tufariello'89
 A;Note: due to a stop codon between the alternative initiators the e antigen precursor
 C;Genetics:
 A;Gene: C
 C;Superfamily: hepatitis B virus core antigen
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 Db 128 TPPAYRPPNAPIL 140

RESULT 12

S53166
 core antigen - hepatitis B virus (isolate patient Tedde'89)

N:Alternate names: HBC antigen

N:Contains: core antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Tedde'89

C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C:Accession: S53166

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53166

A:Molecule type: DNA

A:Residues: 1-183 <LAI>

A:Cross-references: EMBL:X85274; NID:g736053; PIDN:CAA59568.1; PID:g736056

A:Experimental source: isolate patient Tedde'89

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 Db 128 TPPAYRPPNAPIL 140

RESULT 13

S53169

core antigen - hepatitis B virus (isolate patient Muresu'89)

N:Alternate names: HBC antigen

N:Contains: core antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Muresu'89

C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C:Accession: S53169

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53169

A:Molecule type: DNA

A:Residues: 1-183 <LAI>

A:Cross-references: EMBL:X85275; NID:g736057; PIDN:CAA59571.1; PID:g736060

A:Experimental source: isolate patient Muresu'89

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 Db 128 TPPAYRPPNAPIL 140

RESULT 14

S53172

core antigen - hepatitis B virus (isolate patient Urtis'89)

N:Alternate names: HBC antigen

N:Contains: core antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Urtis'89
 C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C:Accession: S53172
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53172
 A:Molecule type: DNA
 A:Residues: 1-183 <LAI>
 A:Cross-references: EMBL:X85276; NID:g736061; PIDN:CAA59574.1; PID:g736064
 A:Experimental source: isolate patient Urtis'89
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 Db 128 TPPAYRPPNAPIL 140

RESULT 15

S53175

core antigen - hepatitis B virus (isolate patient Boi'90)

N:Alternate names: HBC antigen

N:Contains: core antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Boi'90

C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C:Accession: S53175

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53175

A:Molecule type: DNA

A:Residues: 1-183 <LAI>

A:Cross-references: EMBL:X85277; NID:g736065; PIDN:CAA59577.1; PID:g736068

A:Experimental source: isolate patient Boi'90

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 Db 128 TPPAYRPPNAPIL 140

Search completed: August 9, 2004, 13:29:18

Job time : 16 secs


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FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21095 MW; ED2DA1DB07FB596D CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 2
CORR HPBVJ
ID CORR HPBVJ STANDARD; PRT; 183 AA.
AC P1735L;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adw / strain Japan/PJW233).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10413;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.,
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).

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-----
DR EMBL; D00329; -; NOT ANNOTATED_CDS.
DR PIR; A28925; NKVLJ1.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5F5AF5E160 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 3
CORR HPBVL
ID CORR HPBVL STANDARD; PRT; 183 AA.
AC P1290L;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258473; PubMed=2638576;

```

```

RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
RA Harrison T.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee.";
RL J. Gen. Virol. 69:1383-1389(1988).

-----
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-----
DR EMBL; D00220; BAA00157.1; -
DR PIR; A28885; NKVLCP.
DR PDB; 1HHH; 31-OCT-93.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat; 3D-structure.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 20959 MW; 923DCB94A33FC0E8 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 4
CORR HPBVO
ID CORR HPBVO STANDARD; PRT; 183 AA.
AC P17392;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adw / strain Okinawa/PODW282).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.,
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).

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-----
DR EMBL; D00330; -; NOT ANNOTATED_CDS.
DR PIR; B28925; NKVLJ2.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21081 MW; 66BDB2633122930C CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OX NCBI_TaxID=10419;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8102115; PubMed=399329;
RA Pasek M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,
EA Leadbetter G., Murray K.,
RT "Hepatitis B virus genes and their expression in E. coli."
RL Nature 282:575-579 (1979).

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DR EMBL; J02202; AAA45486.1; -;
DR EMBL; A08967; CAA00816.1; -;
DR PIR; B93217; NKVLA2.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
DR Core protein; Repeat.
KW REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21042 MW; 545ED0E5527F26C CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
DB 128 TTPAYRPPNAPIL 140

RESULT 7
CORA HPBV2
ID CORA HPBV2 STANDARD; PRT; 185 AA.
AC P03149;
DT 21-JUL-1986 (Rel. 01, Created)
DI 01-AUG-1992 (Rel. 23, Last sequence update)
DI 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw2).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
DR Core protein; Repeat.
KW REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21304 MW; 31F4DC338B507E19 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
DB 128 TTPAYRPPNAPIL 140

RESULT 8
CORA HPBVW
ID CORA HPBVW STANDARD; PRT; 185 AA.
AC P03149;

OX NCBI_TaxID=10419;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8102115; PubMed=399329;
RA Pasek M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,
EA Leadbetter G., Murray K.,
RT "Hepatitis B virus genes and their expression in E. coli."
RL Nature 282:575-579 (1979).

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DR EMBL; J02202; AAA45486.1; -;
DR EMBL; A08967; CAA00816.1; -;
DR PIR; B93217; NKVLA2.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
DR Core protein; Repeat.
KW REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21042 MW; 545ED0E5527F26C CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
DB 128 TTPAYRPPNAPIL 140

RESULT 7
CORA HPBV2
ID CORA HPBV2 STANDARD; PRT; 185 AA.
AC P03149;
DT 21-JUL-1986 (Rel. 01, Created)
DI 01-AUG-1992 (Rel. 23, Last sequence update)
DI 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw2).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
DR Core protein; Repeat.
KW REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21304 MW; 31F4DC338B507E19 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
DB 128 TTPAYRPPNAPIL 140

RESULT 8
CORA HPBVW
ID CORA HPBVW STANDARD; PRT; 185 AA.
AC P03149;

OX NCBI_TaxID=10419;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8102115; PubMed=399329;
RA Pasek M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,
EA Leadbetter G., Murray K.,
RT "Hepatitis B virus genes and their expression in E. coli."
RL Nature 282:575-579 (1979).

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DR EMBL; J02202; AAA45486.1; -;
DR EMBL; A08967; CAA00816.1; -;
DR PIR; B93217; NKVLA2.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
DR Core protein; Repeat.
KW REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21042 MW; 545ED0E5527F26C CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
DB 128 TTPAYRPPNAPIL 140

RESULT 7
CORA HPBV2
ID CORA HPBV2 STANDARD; PRT; 185 AA.
AC P03149;
DT 21-JUL-1986 (Rel. 01, Created)
DI 01-AUG-1992 (Rel. 23, Last sequence update)
DI 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw2).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
DR Core protein; Repeat.
KW REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21304 MW; 31F4DC338B507E19 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
DB 128 TTPAYRPPNAPIL 140

RESULT 8
CORA HPBVW
ID CORA HPBVW STANDARD; PRT; 185 AA.
AC P03149;

OX NCBI_TaxID=10419;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8102115; PubMed=399329;
RA Pasek M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,
EA Leadbetter G., Murray K.,
RT "Hepatitis B virus genes and their expression in E. coli."
RL Nature 282:575-579 (1979).

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DR EMBL; J02202; AAA45486.1; -;
DR EMBL; A08967; CAA00816.1; -;
DR PIR; B93217; NKVLA2.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
DR Core protein; Repeat.
KW REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21042 MW; 545ED0E5527F26C CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
DB 128 TTPAYRPPNAPIL 140

RESULT 7
CORA HPBV2
ID CORA HPBV2 STANDARD; PRT; 185 AA.
AC P03149;
DT 21-JUL-1986 (Rel. 01, Created)
DI 01-AUG-1992 (Rel. 23, Last sequence update)
DI 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw2).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=

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DB 21-JUL-1986 (Rel. 01, Created)
DB 21-JUL-1986 (Rel. 01, Last sequence update)
DB 01-OCT-1989 (Rel. 12, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw).
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=106821;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RL DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757(1983).
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CC -----
CC EMBL; V00866; ; NOT ANNOTATED CDS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21394 MW; B86A90D541BA70F9 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
DB 128 TPPAYRPPNPAPIL 140

RESULT 9
CORA HPBVF
ID CORA HPBVF STANDARD; PRT; 195 AA.
AC P29178;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw2 variant sf).
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169850; PubMed=2307406;
RA Bhat R.A., Ulrich P.P., Vyas G.N.;
RT "Molecular characterization of a new variant of hepatitis B virus in
RL a persistently infected homosexual man.";
RL Hepatology 11:271-276(1990).
DR PIR; A37182; NKVLH3.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 174 181
FT REPEAT 182 189
SQ SEQUENCE 195 AA; 22461 MW; E2B166F879CB7CRC64;

Query Match 100.0%; Score 74; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
DB 128 TPPAYRPPNPAPIL 140

RESULT 10
CORA HPBVA
ID CORA HPBVA STANDARD; PRT; 211 AA.
AC P24023;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain alpha1).
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90266476; PubMed=2345966;
RA Tong S., Li J., Witvitski L., Trepo C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
RL associated with viral variants containing an inactive pre-C region.";
RL Virology 176:596-603(1990).
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CC -----
CC EMBL; M32138; ; NOT ANNOTATED CDS.
DR PIR; A34773; NKVLAL.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 183 190
FT REPEAT 198 206
SQ SEQUENCE 211 AA; 24208 MW; B774AC72B65C75AB CRC64;

Query Match 100.0%; Score 74; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
DB 156 TPPAYRPPNPAPIL 168

RESULT 11
CORA HPBVT
ID CORA HPBVT STANDARD; PRT; 212 AA.
AC Q05495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RL that expresses HBV surface antigen subtype adw4.";
RL J. Gen. Virol. 74:1627-1632(1993).
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DR EMBL; X69798; CAA49452.1; -;
 DR F02227; JQ2227.
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT DOMAIN 178 204 ARG-RICH.
 FT REPEAT 184 203 3 X 5 AA REPEATS OF S-P-R-R-R.
 FT REPEAT 184 188 1.
 FT REPEAT 191 195 2.
 FT REPEAT 199 203 3.
 SQ SEQUENCE 212 AA; 24234 MW; F832610DB7C36FD2 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 0.00061;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNPAPIL 13
 |||||
 Db 157 TPPAYRPPNPAPIL 169

RESULT 12

CORA_HPBV9
 ID CORA_HPBV9 STANDARD; PRT; 214 AA.
 AC P17099;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE Core antigen.

CC
 OS Hepatitis B virus (subtype adw / strain 991).
 OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10410;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Koehel H.G., Schueler A., Lottmann S., Thomssen R.;
 RA Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
 RL

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DR EMBL; X51370; CAA36232.1; -;
 DR F03081; NKVLC5.
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT REPEAT 193 200
 FT REPEAT 201 208
 SQ SEQUENCE 214 AA; 24722 MW; 2D668333BC5AFB8C CRC64;

Query Match 100.0%; Score 74; DB 1; Length 214;
 Best Local Similarity 100.0%; Pred. No. 0.00062;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNPAPIL 13
 |||||
 Db 157 TPPAYRPPNPAPIL 169

RESULT 13

CORA_WHV8
 ID CORA_WHV8 STANDARD; PRT; 187 AA.

P06433;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-OCT-1989 (Rel. 12, Last annotation update)
 DE Core antigen.

CC
 OS Woodchuck hepatitis virus 8 (WHV 8).
 OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10433;
 RN [1]
 RP SEQUENCE FROM N.A.

EX MEDLINE=86082931; PubMed=3855246;
 RA Kodama K., Ogasawara N., Yoshikawa H., Murakami S.;
 RA "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
 RT evolutionary relationship between hepadnaviruses.";
 RL J. Virol. 56:978-986(1985).

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DR EMBL; M11082; AAA19185.1; -;
 DR F03714; NKVLC2.
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.

KW Core protein; Repeat.
 FT REPEAT 166 173
 FT REPEAT 174 181
 SQ SEQUENCE 187 AA; 21579 MW; D4BC446FF7163165 CRC64;

Query Match 82.4%; Score 61; DB 1; Length 187;
 Best Local Similarity 84.6%; Pred. No. 0.04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNPAPIL 13
 |||||
 Db 128 TPPAYRPPNPAPIL 140

RESULT 14

CORA_WHV1
 ID CORA_WHV1 STANDARD; PRT; 188 AA.
 AC P03152;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Core antigen.

CC
 OS Woodchuck hepatitis virus 1 (WHV 1),
 OS Woodchuck hepatitis virus 7 (WHV 7),
 OS Woodchuck hepatitis virus 59 (WHV 59), and
 OS Woodchuck hepatitis virus 8 (infectious clone) (WHV 8).
 OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10430, 10432, 10431, 10434;
 RN [1]
 RP SEQUENCE FROM N.A.

RC SPECIES=Woodchuck hepatitis virus 1;
 RX MEDLINE=82216969; PubMed=7086958;
 RA Galibert F., Chen T.N., Mandart E.;
 RA "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
 RT comparison with the hepatitis B virus sequence.";
 RL J. Virol. 41:51-65(1982).

CC
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Woodchuck hepatitis virus 7, and Woodchuck hepatitis virus 59;
 RX MEDLINE=88101359; PubMed=3336938;
 RA Cohen J.I., Miller R.H., Rosenblum B., Denniston K., Gerin J.L.,
 RA Purcell R.H.;
 RA "Sequence comparison of woodchuck hepatitis virus replicative forms

RT shows conservation of the genome." ;
 RL Virology 162:12-20(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=woodchuck hepatitis virus 8 (infectious clones);
 RX MEDLINE=89184524; PubMed=2928306;
 RA Girones R., Cote P.J., Hornbuckle W.B., Tennant B.C., Gerin J.L.,
 RA Pucell R.H., Miller R.H.;
 RT "Complete nucleotide sequence of a molecular clone of woodchuck
 RL hepatitis virus that is infectious in the natural host." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1846-1849(1989).
 CC -----
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 CC -----
 CC EMBL; J02442; AAA46761.1; -
 DR EMBL; M18752; AAA46769.1; -
 DR EMBL; M19183; AAA46765.1; -
 DR EMBL; J04514; AAA46772.1; -
 DR PIR; C32397; NKVLC.
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 KW Core protein; Repeat.
 FT REPEAT 167 174
 FT REPEAT 175 182
 SQ SEQUENCE 188 AA; 21693 MW; 1F4454D0A7B7CE42 CRC64;

 Query Match 82.4%; Score 61; DB 1; Length 188;
 Best Local Similarity 84.6%; Pred. No. 0.04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 TPPAYRPPNPAPIL 13
 || |||||
 Db 128 TPAPYRPPNPAPIL 140

 RESULT 15
 CORA_HPBGS STANDARD; PRT; 217 AA.
 AC P03153;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-JAN-1990 (Rel. 13, Last annotation update)
 DE Core antigen.
 GN C.
 OS Ground squirrel hepatitis virus (GSV).
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84267998; PubMed=6086950;
 RA Seeger C., Ganem D., Varmus H.E.;
 RT "Nucleotide sequence of an infectious molecularly cloned genome of
 RL ground squirrel hepatitis virus." ;
 RL J. Virol. 51:367-375(1984).
 CC -----
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 CC -----
 CC EMBL; K02715; AAA46755.1; -
 DR PIR; A03715; NKVLS.
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.

KW Core protein; Repeat.
 FT REPEAT 196 203
 FT REPEAT 204 211
 SQ SEQUENCE 217 AA; 25189 MW; DF489467355EC11A CRC64;

 Query Match 82.4%; Score 61; DB 1; Length 217;
 Best Local Similarity 84.6%; Pred. No. 0.046;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 TPPAYRPPNPAPIL 13
 || |||||
 Db 157 TPAPYRPPNPAPIL 169

 Search completed: August 9, 2004, 13:28:04
 Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2004, 13:27:00 ; Search time 35 Seconds
(without alignments)
117.192 Million cell updates/sec

Title: US-09-277-074-9

Sequence: 1 TTPAYRPPNAPIL 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	96	12	Q9YQ42 hepatitis b
2	74	100.0	96	12	Q9YJM3 hepatitis b
3	74	100.0	113	12	Q80J61 hepatitis b
4	74	100.0	130	12	Q8QP24 hepatitis b
5	74	100.0	130	12	Q8QPI1 hepatitis b
6	74	100.0	130	12	Q8JSV0 hepatitis b
7	74	100.0	130	12	Q8QP22 hepatitis b
8	74	100.0	130	12	Q8JSW1 hepatitis b
9	74	100.0	130	12	Q8JSV2 hepatitis b
10	74	100.0	130	12	Q8JSV9 hepatitis b
11	74	100.0	130	12	Q8QP19 hepatitis b
12	74	100.0	130	12	Q8JSV1 hepatitis b
13	74	100.0	130	12	Q8JSW5 hepatitis b
14	74	100.0	130	12	Q8JSW9 hepatitis b
15	74	100.0	130	12	Q8QP32 hepatitis b
16	74	100.0	130	12	Q8JSV3 hepatitis b

17	74	100.0	130	12	Q8QP23	hepatitis b
18	74	100.0	130	12	Q8QP31	hepatitis b
19	74	100.0	130	12	Q8QP25	hepatitis b
20	74	100.0	130	12	Q8QP16	hepatitis b
21	74	100.0	130	12	Q8QP21	hepatitis b
22	74	100.0	130	12	Q8QP27	hepatitis b
23	74	100.0	130	12	Q8JSW3	hepatitis b
24	74	100.0	130	12	Q8JSX0	hepatitis b
25	74	100.0	130	12	Q8QP29	hepatitis b
26	74	100.0	130	12	Q8QP34	hepatitis b
27	74	100.0	130	12	Q8JSW7	hepatitis b
28	74	100.0	130	12	Q8JSX5	hepatitis b
29	74	100.0	130	12	Q8JSV5	hepatitis b
30	74	100.0	130	12	Q8JSW8	hepatitis b
31	74	100.0	130	12	Q8QP30	hepatitis b
32	74	100.0	130	12	Q8QP17	hepatitis b
33	74	100.0	130	12	Q8JSW2	hepatitis b
34	74	100.0	130	12	Q8JSX1	hepatitis b
35	74	100.0	130	12	Q8JSV6	hepatitis b
36	74	100.0	130	12	Q8QP13	hepatitis b
37	74	100.0	130	12	Q8JSW4	hepatitis b
38	74	100.0	130	12	Q8QP18	hepatitis b
39	74	100.0	130	12	Q8QP26	hepatitis b
40	74	100.0	130	12	Q8JSV4	hepatitis b
41	74	100.0	130	12	Q8JSW6	hepatitis b
42	74	100.0	130	12	Q8QP28	hepatitis b
43	74	100.0	130	12	Q8QP15	hepatitis b
44	74	100.0	130	12	Q8JSW0	hepatitis b
45	74	100.0	130	12	Q8JSX3	hepatitis b

ALIGNMENTS

RESULT 1

Q9YQ42 PRELIMINARY; PRT; 96 AA.
AC Q9YQ42;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Core antigen (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=genotype D;
RX MEDLINE=20381124; PubMed=10921962;
RA Petrosillo N., Ippolito G., Solforosi L, Varaldo P.E., Clementi M.,
RA Manzin A.;
RT "Molecular epidemiology of an outbreak of fulminant Hepatitis B.";
RL J. Clin. Microbiol. 38:2975-2981(2000).
DR EMBL; AJ010001; CAA08950.1;
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON TER 1
SQ SEQUENCE 96 AA; 11428 MW; D46972F6440979BE CRC64;

Query Match 100.0%; Score 74; DB 12; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPAYRPPNAPIL 13
Db 41 TTPAYRPPNAPIL 53

RESULT 2

Q9YJM3 PRELIMINARY; PRT; 96 AA.
ID Q9YJM3
AC Q9YJM3;

```

DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Core antigen (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GENOTYPE D;
RA Manzin A.;
RT "An outbreak of fulminant hepatitis B in a haematologic unit (Pesaro, Italy), part 2."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010007; CAA08962.1; -
DR EMBL; AJ009994; CAA08936.1; -
DR EMBL; AJ009995; CAA08938.1; -
DR EMBL; AJ009996; CAA08940.1; -
DR EMBL; AJ009997; CAA08942.1; -
DR EMBL; AJ009998; CAA08944.1; -
DR EMBL; AJ009999; CAA08946.1; -
DR EMBL; AJ010000; CAA08948.1; -
DR EMBL; AJ010002; CAA08952.1; -
DR EMBL; AJ010003; CAA08954.1; -
DR EMBL; AJ010004; CAA08956.1; -
DR EMBL; AJ010005; CAA08958.1; -
DR EMBL; AJ010006; CAA08960.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER
SQ SEQUENCE 96 AA; 11443 MW; FBA862E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 12; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
Db 41 TPPAYRPPNPAPIL 53

RESULT 3
Q80J61 PRELIMINARY; PRT; 113 AA.
ID Q80J61
AC Q80J61
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Core protein.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7-2;
RA Luo K., Liu Z., He H., Liang W., Peng J., Dai W., Hou J.;
RT "The putative recombination of hepatitis B virus genotype B with pre-C/C of genotype C."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY217370; AAO63544.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
SQ SEQUENCE 113 AA; 13068 MW; 3A0E460F2038C680 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
Db 58 TPPAYRPPNPAPIL 70

RESULT 4
Q8QP24 PRELIMINARY; PRT; 130 AA.
ID Q8QP24
AC Q8QP24
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Core protein (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=45B;
RA Dumpis U., Jansons J., Solominskaya I., Michailova M., Pumpens P.;
RT "Containment of the outbreak of Hepatitis B and C infection in a Latvian pediatric oncology ward."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079230; AAM11934.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER
SQ SEQUENCE 130 AA; 15151 MW; E32DD1DB4E4D51DC CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
Db 75 TPPAYRPPNPAPIL 87

RESULT 5
Q8QP11 PRELIMINARY; PRT; 130 AA.
ID Q8QP11
AC Q8QP11
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Core protein (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9latvia;
RA Dumpis U., Jansons J., Solominskaya I., Michailova M., Pumpens P.;
RT "Containment of the outbreak of Hepatitis B and C infection in a Latvian pediatric oncology ward."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079243; AAM11947.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER
SQ SEQUENCE 130 AA; 15065 MW; 45D8AB909ECD9BAE CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
Db 75 TPPAYRPPNPAPIL 87

RESULT 6
Q8JSV0 PRELIMINARY; PRT; 130 AA.
ID Q8JSV0
AC Q8JSV0

```


OX NCBI_TaxID=10407;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=LR4.1/A;
 RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
 RT "Genotype mixtures of hepatitis B virus in patients treated with
 interferon."
 RL J. Infect. Dis. 0:0-0(2002).
 DR EMBL; AF474394; AAM70072.1; -;
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 14708 MW; 0B393223D37604D1 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 111 TPPAYRPPNAPIL 123

RESULT 11
 Q8QPI9 PRELIMINARY; PRT; 130 AA.
 AC Q8QPI9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Core protein (Fragment).
 GN C.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dumpis U., Jansons J., Solominskaya I., Michailova M., Pumpens P.;
 RT "Containment of the outbreak of Hepatitis B and C infection in a
 Latvian pediatric oncology ward."
 RL Submitted (FEF-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY079235; AAM11939.1;
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 15136 MW; 04BA4FDCD7DD51D8 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 75 TPPAYRPPNAPIL 87

RESULT 12
 Q8JSV1 PRELIMINARY; PRT; 130 AA.
 AC Q8JSV1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Core protein (Fragment).
 GN C.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SR6.2/X2;
 RT Hannoun C., Krogsgaard K., Horal P., Lindh M.;

RT "Genotype mixtures of hepatitis B virus in patients treated with
 interferon."
 RL J. Infect. Dis. 0:0-0(2002).
 DR EMBL; AF474402; AAM70080.1; -;
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 14708 MW; 0B393223D37604D1 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 111 TPPAYRPPNAPIL 123

RESULT 13
 Q8JSW5 PRELIMINARY; PRT; 130 AA.
 AC Q8JSW5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Core protein (Fragment).
 GN C.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rel4.3/X2;
 RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
 RT "Genotype mixtures of hepatitis B virus in patients treated with
 interferon."
 RL J. Infect. Dis. 0:0-0(2002).
 DR EMBL; AF474388; AAM70066.1; -;
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 14628 MW; 48EF8BE4C0D21408 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 111 TPPAYRPPNAPIL 123

RESULT 14
 Q8JSW9 PRELIMINARY; PRT; 130 AA.
 AC Q8JSW9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Core protein (Fragment).
 GN C.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rel4.1/A1;
 RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
 RT "Genotype mixtures of hepatitis B virus in patients treated with
 interferon."
 RL J. Infect. Dis. 0:0-0(2002).

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DR EMBL; AF474384; AM70062.1; -.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 14744 MW; 4792P0C7F1C0D8A CRC64;

Query Match      100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
DB 111 TPPAYRPPNPAPIL 123

RESULT 15
Q8QF32 PRELIMINARY; PRT; 130 AA.
AC O8QF32;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Core protein (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2T;
RA Dumpis U., Jansons J., Solominskaya I., Michailova M., Pumpens P.;
RT "Containment of the outbreak of Hepatitis B and C infection in a
RT Latvian pediatric oncology ward.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079222; AAU1926.1; -.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15137 MW; E4B44FDCD7D351DC CRC64;

Query Match      100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
DB 75 TPPAYRPPNPAPIL 87

Search completed: August 9, 2004, 13:28:52
Job time : 36 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:26:45 ; Search time 50 Seconds

(without alignments)
73.462 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPAYRPPNAPIL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 383904

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001s.*
 - 5: Geneseq2002s.*
 - 6: Geneseq2003as.*
 - 7: Geneseq2003bs.*
 - 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	13	2 AAR33501	Aar33501 T helper
2	74	100.0	13	2 AAR78929	Aar78929 HBC 128-1
3	74	100.0	13	2 AAW39439	Aaw39439 Mouse H-2
4	74	100.0	13	2 AAW50117	Aaw50117 Pan DR b1
5	74	100.0	13	3 AAY52556	Aay52556 HBV core
6	74	100.0	13	4 AAG64542	Aag64542 T-helper
7	74	100.0	13	4 AAE02681	Aae02681 Hepatitis
8	74	100.0	13	4 AAE00471	Aae00471 Hepatitis
9	74	100.0	13	4 AAG62426	Aag62426 Immunogen
10	74	100.0	13	4 AAB82775	Aab82775 Hepatitis
11	74	100.0	13	4 AAU00614	Aau00614 H-2 I-Ab-
12	74	100.0	13	5 AAU70851	Aau70851 Hepatitis
13	74	100.0	13	5 ABB76787	Abb76787 HBV pepti
14	74	100.0	13	5 ABG62860	Abg62860 Antigenic
15	74	100.0	13	5 ABP52344	Abp52344 TH epitop
16	74	100.0	13	5 ABP52307	Abp52307 T helper
17	74	100.0	13	5 ABP53350	Abp53350 TH epitop
18	74	100.0	13	5 ABP51503	Abp51503 T helper
19	74	100.0	13	6 ABR44095	Abp44095 HBV core
20	74	100.0	13	6 ABP98778	Abp98778 HBV core
21	74	100.0	13	6 AAO22990	Aao22990 p128-40 I
22	74	100.0	13	6 ABU63009	Abu63009 HBV core
23	74	100.0	13	7 ABC21494	Abc21494 Hepatitis
24	74	100.0	13	7 ADC85105	Adc85105 HBV assoc
25	74	100.0	13	7 ADD35647	Add35647 Hepatitis

26	69	93.2	12	1 AAR80957	Aap80957 T cell st
27	69	93.2	13	6 ADA51351	Ada51351 Hepatitis
28	65	87.8	11	5 ABJ06979	Abj06979 Hepatitis
29	65	87.8	11	5 ABJ07803	Abj07803 Hepatitis
30	65	87.8	12	6 ADA51350	Ada51350 Hepatitis
31	65	87.8	13	6 ADA51364	Ada51364 Hepatitis
32	64	86.5	12	6 ADA51337	Ada51337 Hepatitis
33	64	86.5	13	6 ADA51338	Ada51338 Hepatitis
34	62	83.8	11	5 ABJ07363	Abj07363 Hepatitis
35	62	83.8	11	5 ABJ06223	Abj06223 Hepatitis
36	61	82.4	11	6 ADA51349	Ada51349 Hepatitis
37	61	82.4	12	6 ADA51363	Ada51363 Hepatitis
38	61	82.4	13	6 ADA51377	Ada51377 Hepatitis
39	60	81.1	11	6 ADA51336	Ada51336 Hepatitis
40	59	79.7	10	2 AAY47999	Aay47999 Immunogen
41	59	79.7	10	5 ABJ07000	Abj07000 Hepatitis
42	59	79.7	10	5 ABJ07724	Abj07724 Hepatitis
43	59	79.7	11	5 ABJ06294	Abj06294 Hepatitis
44	59	79.7	11	5 ABJ08210	Abj08210 Hepatitis
45	59	79.7	11	5 ABJ07371	Abj07371 Hepatitis

ALIGNMENTS

RESULT 1
AAR33501
ID AAR33501 standard; peptide; 13 AA.

- AC AAR33501;
- XX
- DT 25-MAR-2003 (revised)
- DT 01-JUL-1993 (first entry)
- XX
- DE T helper peptide HBC 128-140.
- XX
- KW Hepatitis B virus; HBV; core antigen; MHC class I; chronic; acute;
- KW infection; identification; HLA-restricted.
- XX
- OS Synthetic.
- XX
- XX WO9303764-A1.
- XX
- PD 04-MAR-1993.
- XX
- PF 26-AUG-1992; 92WO-US007218.
- XX
- PR 26-AUG-1991; 91US-00749568.
- PR 29-JAN-1992; 92US-00827682.
- PR 27-APR-1992; 92US-00874491.
- XX
- PA (CYTB-) CYTEL CORP.
- XX
- PI Vitello MA, Chesnut RW;
- XX
- DR WPI; 1993-093728/11.
- XX
- PT Cytotoxic T-lymphocyte stimulating peptide(s) - derived from hepatitis B virus useful for treating, preventing and diagnosing infection.
- XX
- PS Disclosure; Page 21; 89pp; English.
- XX
- CC This is a T helper epitope peptide, the sequence of which is derived from hepatitis B virus (HBV) core antigen amino acids 128-140. It may be used in a conjugate with cytotoxic T-lymphocyte stimulating (CTL) peptides to enhance an individual's immunity by providing cell-mediated immunity and protective antibodies. (Updated on 25-MAR-2003 to correct PN field.)
- XX
- SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 2
 AAR78929
 ID AAR78929 standard; peptide; 13 AA.
 XX
 AC AAR78929;
 DT 25-MAR-2003 (revised)
 DT 27-MAR-1996 (first entry)
 XX
 DE HBC 128-140 cytotoxic T lymphocyte epitope.
 XX
 KW HBC 128-140; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte;
 KW antigens; treatment; disease prevention; hepatitis B.
 XX
 OS Hepatitis B virus.
 XX
 FN WO9522317-A1.
 XX
 PD 24-AUG-1995.
 XX
 PF 16-FEB-1995; 95WO-US002121.
 XX
 PR 16-FEB-1994; 94US-00197484.
 XX
 PA (CYTE-) CYTEL CORP.
 PI Vitello MA, Chesnut RW, Sette AD, Celis E, Grey H;
 XX
 DR WPI; 1995-302545/39.
 XX
 PT Compn. inducing cytotoxic T lymphocyte response to pref. viral,
 PT bacterial, parasitic or tumour antigens - useful in the treatment and
 PT prevention of diseases associated with the antigen e.g. hepatitis B.
 XX
 PS Example 4; Page 52; 109pp; English.
 CC A compen. which induces a cytotoxic T lymphocyte (CTL) response to a
 CC hepatitis B virus (HBV) antigen (Ag) in a mammal comprises, a HBV CTL Ag
 CC response inducing peptide (i.e. AAR78929) and a lipid conjugated helper T
 CC cell inducing peptide. The compn. is useful in the treatment and
 CC prevention of hepatitis B. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 3
 AAW39439
 ID AAW39439 standard; peptide; 13 AA.
 XX
 AC AAW39439;
 DT 11-JUN-1998 (first entry)
 XX
 DE Mouse H-2 I-Ab-restricted HBV core antigen-derived T helper epitope.
 XX
 KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
 KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
 KW disease; anti-tumour; anti-viral.
 XX

OS Synthetic.
 OS Mus sp.
 XX
 PN WO9741440-A1.
 XX
 PD 06-NOV-1997.
 XX
 XX 28-APR-1997; 97WO-NL000229.
 XX
 PR 26-APR-1996; 96EP-00201145.
 PR 23-DEC-1996; 96EP-00203670.
 XX
 XX (UYLE-) RIJCSUNIV LEIDEN.
 PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
 XX
 PI Van Der Burg SH, Kast WM, Toes REM, Offringa R, Melief CJM;
 XX
 DR WPI; 1997-549891/50.
 XX
 PT Method of selecting T cell peptide epitope(s) - by measuring the
 PT stability of HLA class I-peptide complexes on intact B cells.
 XX
 PS Example 2; Page 21; 109pp; English.
 XX
 CC Peptides AAW39430-W39734 are used in a novel method for the selection of
 CC immunogenic T-cell peptide epitopes present in polypeptide antigens.
 CC Peptide AAW39439 is a mouse H-2 I-Ab restricted HBV core antigen-derived
 CC T helper epitope which is injected into HLA-A*0201Kb transgenic mice. The
 CC method involves the identification of peptide sequences capable of
 CC binding to an HLA (human leukocyte antigen) class I molecule and
 CC measuring the binding of this epitope peptide to the HLA class I peptide.
 CC The stability of binding of the peptide and MHC (major histocompatibility
 CC complex) class I molecule is measured on intact human B cells carrying
 CC the MHC molecule at their cell surfaces. The method can be used to select
 CC peptide epitopes for generating vaccines against a disease associated
 CC with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are
 CC especially T-cell peptide epitopes with strong anti-tumour and anti-viral
 CC immune responses
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 4
 AAW50117
 ID AAW50117 standard; peptide; 13 AA.
 XX
 AC AAW50117;
 DT 30-JUN-1998 (first entry)
 XX
 DE Pan DR binding peptide (14).
 XX
 KW Pan DR binding peptide; antigen binding site; MHC molecule; DR locus.
 XX
 OS Synthetic.
 XX
 PN US5736142-A.
 XX
 PD 07-APR-1998.
 XX
 PF 14-SEP-1994; 94US-00305871.
 XX
 PR 14-SEP-1993; 93US-00121101.
 XX
 PA (CYTE-) CYTEL CORP.

XX Sidney J, Sette A, Alexander JL, Gaeta F, Grey HM;
 XX WPI; 1998-239154/21.
 XX
 XX Peptides that bind to MHC molecules of all DR alleles - inhibiting or
 PT inducing MHC Class II mediated activation of T cells.
 XX
 XX Example 5; Col 35-36; 29pp; English.
 XX
 XX The present sequence, a pan DR binding peptide, is capable of binding
 CC antigen binding sites on MHC molecules, which are encoded by most of the
 CC alleles of a DR locus. The peptide can be used to inhibit or induce MHC
 CC Class II mediated activation of T-cells or helper T-cells, which
 CC themselves mediate a CTL response. The peptide can be used in mammals,
 CC especially humans, to inhibit T-cell-mediated events involved in
 CC allograft rejection, allergic responses and autoimmunity and as a vaccine
 CC adjuvant for enhancing an immune response against an administered
 CC immunogen. The peptide can be used with other immunogens to treat, e.g.
 CC prostate cancer, hepatitis B, hepatitis C, AIDS, renal and cervical
 CC carcinoma, lymphoma, CMV and condyloma acuminatum
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNAPIL 13
 Db |||||
 1 TPPAYRPPNAPIL 13
 RESULT 5
 AAY52556
 ID AAY52556 standard; peptide; 13 AA.
 AC AAY52556;
 XX
 XX 06-AUG-2003 (revised)
 DT 28-FEB-2000 (first entry)
 XX
 XX HBV core antigen MHC class II epitope, encoded by I80T fusion gene.
 XX
 XX Chimeric; pan DR epitope; expression vector; promoter;
 KW major histocompatibility complex; MHC; targeting; peptide; epitope;
 KW antigen; presentation; class I; cytosolic pathway; endoplasmic reticulum;
 KW class II; extracellular antigen; endocytic pathway; helper T lymphocyte;
 KW HTL; universal epitope; cytotoxic T lymphocyte; CTL; immune response;
 KW immunogenicity; assay; vaccine; immunity; infection; pathogen; virus;
 KW HIV; HBV; HCV; hepatitis B; hepatitis C; bacterium; protozoan;
 KW tumour cell; autoimmune disease; activation; antiviral; antimalarial;
 KW immunoprotective; core antigen.
 XX
 OS Synthetic.
 OS Hepatitis B virus.
 XX
 XX WO9958658-A2.
 XX
 XX 18-NOV-1999.
 XX
 XX 13-MAY-1999; 99WO-US010646.
 PF
 XX 13-MAY-1998; 98US-00078904.
 PR
 XX 15-MAY-1998; 98US-0085751P.
 PR
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
 PI Chesnut RW;
 XX
 XX WPI; 2000-039103/03.
 DR
 XX

PT Expression vectors encoding major histocompatibility targeting sequence,
 PT used as, e.g. tumor vaccines.
 XX
 XX Example 1; Page 36; 130pp; English.
 XX
 XX This sequence represents a hepatitis B virus (HBV) core antigen MHC class
 CC II epitope, encoded by the I80T fusion gene (AAZ38617), used in an
 CC exemplification of the present invention. The invention relates to a
 CC novel expression vector comprising a promoter operably linked to a fusion
 CC gene encoding a major histocompatibility complex (MHC) targeting
 CC sequence, and two or more heterologous peptide epitopes. The MHC
 CC targeting sequence may be a class I targeting sequence, which directs
 CC an MHC class I epitope to a cytosolic pathway or to the endoplasmic
 CC reticulum, or an MHC class II targeting sequence, which directs
 CC extracellular antigens to enter the endocytic pathway to be processed
 CC into antigen peptides for presentation on MHC class II molecules. The
 CC heterologous epitopes may comprise either helper T lymphocyte (HTL)
 CC epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL
 CC epitope, such as a pan DR epitope (PADRE). The vectors are useful for
 CC stimulating an immune response in vivo, as well as for use in assaying
 CC the human immunogenicity of a human T cell peptide epitope in vivo in a
 CC non-human mammal. They provide a nucleic acid vaccine for enhancing
 CC immunity against infectious pathogens, such as viruses (e.g., HIV,
 CC hepatitis B (HBV) and hepatitis C (HCV)), bacteria, protozoa (e.g.,
 CC Plasmodium falciparum, the cause of malaria) and also tumour cells and
 CC autoimmune diseases. Universal MHC class II epitopes are advantageously
 CC combined with other MHC class I and class II epitopes to increase the
 CC number of cells that are activated in response to a given antigen and
 CC provide a broader population coverage of MHC-reactive alleles. (Updated
 CC on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNAPIL 13
 Db |||||
 1 TPPAYRPPNAPIL 13
 RESULT 6
 AAG64542
 ID AAG64542 standard; peptide; 13 AA.
 AC AAG64542;
 XX
 XX 22-OCT-2001 (first entry)
 DT
 XX T-helper epitope peptide.
 DE Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
 XX human immunodeficiency virus; vaccine; T-helper.
 KW
 XX Synthetic.
 OS
 OS WO200155177-A2.
 XX
 XX 02-AUG-2001.
 XX
 XX 29-JAN-2001; 2001WO-DK000059.
 PF
 XX 28-JAN-2000; 2000EP-00610017.
 PR
 XX 31-JAN-2000; 2000US-0179333P.
 PR
 XX (STAT-) STATENS SERUM INST.
 PA
 XX Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
 PI WPI; 2001-476184/51.
 XX
 XX The generation of cytotoxic T cell lymphocytes epitopes for use in anti-

PT HIV vaccines.

PS Example 7; Page 42; 383pp; English.

XX The invention relates to identification of cytotoxic T cell lymphocyte

CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL

CC are a major protective mechanism against viral diseases. Antibodies may

CC neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine,

CC in the manufacture of vaccines or diagnostic agents. The present sequence

CC is that of a T-helper epitope peptide useful to the invention

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. NO. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 1 TPPAYRPPNAPIL 13

RESULT 7

AAE02681

ID AAE02681 standard; peptide; 13 AA.

AC AAE02681;

XX

XX 06-AUG-2001 (first entry)

DT Hepatitis B virus HBVc helper peptide.

DE

XX Cytostatic; antibacterial; antifungal; gene therapy; vaccine; antiviral;

XX tumour; epitope; glycoprotein; hepatitis B virus; HBV; immune response;

KW CTL; cytotoxic T lymphocyte; HLA; human leucocyte antigen.

KW

XX Hepatitis B virus.

OS

XX WO200127291-A1.

PN

XX 19-APR-2001.

PD

XX 29-SEP-2000; 2000WO-EP009902.

PF

XX 12-OCT-1999; 99US-0158356P.

PR

XX (INSP) INST PASTEUR.

PA

XX Firat H, Lemonnier F, Langlade-Demoyen P;

PI

XX WPI; 2001-282039/29.

DR

XX New polynucleotide comprising at least one viral, fungal, bacterial, or

PT tumor epitope of an antigen, capable of inducing a cellular response.

PS

XX Example 1; Page 23; 70pp; English.

XX The invention relates to polynucleotide containing at least a part of the

CC coding sequence of the middle glycoprotein of hepatitis B virus (HBV) in

CC which is inserted a DNA sequence coding for an epitope comprising at

CC least one viral, fungal, bacterial, or tumour epitope of an antigen,

CC capable of inducing a cellular response. Nucleic acids and compositions

CC of the invention are useful for inducing in vivo a CTL (cytotoxic T

CC lymphocyte) response against several epitopes of one or more, bacterial,

CC viral, fungal, or tumour antigens. A composition of the invention

CC produces an immune response against HIV antigen and are used in the

CC production of vaccines. The polynucleotides of the invention are also

CC used in gene therapy. The present sequence is hepatitis B virus helper

CC peptide. This peptide is co-injected with human epitopes in order to

CC elicit HLA (human leucocyte antigen) -A2.1-restricted CTL response in

CC mice

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. NO. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 1 TPPAYRPPNAPIL 13

RESULT 8

AAE00471

ID AAE00471 standard; peptide; 13 AA.

XX

AC AAE00471;

XX

XX 19-JUN-2001 (first entry)

DT Hepatitis B virus core (HBVc) tumour epitope peptide.

DE

XX Tumour epitope; cytostatic; immunostimulant; gene therapy;

XX middle glycoprotein; Hepatitis B virus core; cytotoxic response;

KW immune response; cytotoxic T lymphocyte; CTL; HBVc; HLA;

KW human leucocyte antigen.

XX

OS Hepatitis B virus.

XX

XX WO200123577-A2.

PN

XX 05-APR-2001.

PD

XX 29-SEP-2000; 2000WO-EP009900.

PF

XX 30-SEP-1999; 99US-0156945P.

PR

XX (INSP) INST PASTEUR.

PA

XX Firat H, Lemonnier F, Langlade-Demoyen P, Michel M, Suhrbier AA;

PI

XX WPI; 2001-266164/27.

DR

XX Novel polynucleotide having DNA sequence encoding tumor antigen epitope

PT inserted in part of coding sequence of middle glycoprotein of hepatitis B

PT virus, used to induce immune response against tumor-specific antigen.

XX

PS Example 1; Page 13; 36pp; English.

XX The present invention relates to an isolated or purified polynucleotide

CC containing a DNA sequence coding for at least one tumour epitope of a

CC tumour antigen inserted into part of the coding sequence of the middle

CC glycoprotein of the Hepatitis B virus (HBV). The polynucleotide is useful

CC for optionally evaluating cytotoxic responses in the individual's

CC lymphocyte population. It induces an immune response against at least one

CC tumour specific antigen or tissue specific antigen. The vector comprising

CC the polynucleotide induces in vivo, cellular and/or humoral immune

CC response. The composition comprising the polynucleotide induces in vivo,

CC cytotoxic T lymphocyte (CTL) against one or more antigens or epitopes

CC present on the hybrid protein. The polynucleotide is also useful in gene

CC therapy. The present sequence is a Hepatitis B virus core (HBVc) tumour

CC epitope peptide. This peptide elicits HLA (human leucocyte antigen) -A2.1

CC - restricted CTL response in mice

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. NO. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 1 TPPAYRPPNAPIL 13

RESULT 9
AAG62426
ID AAG62426 standard; peptide; 13 AA.
XX
AC AAG62426;
XX
DT 03-SEP-2001 (first entry)
XX
DE Immunogenic peptide HBV core SEQ ID 30.
XX
KW Class I epitope; immunogenic; heteroclitic analogue; immune response;
KW antigen display; viral disease; cancer.
XX
OS Synthetic.
XX
PN WO200136452-A2.
XX
PD 25-MAY-2001.
XX
PF 20-NOV-2000; 2000WO-US031856.
XX
PR 18-NOV-1999; 99US-0156529P.
XX
PR 06-OCT-2000; 2000US-0239008P.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Tangri S, Sette A, Ishioka G;
XX
XX WPI; 2001-355609/37.
XX
XX Enhancing immunogenicity of peptide containing class I epitope, useful
PT for treating cancer, comprises providing (semi-)conservative amino acid
PT substitutions at specified positions of these epitopes.
XX
PS Disclosure; Fig 1A; 96pp; English.
XX
CC This invention relates to a method of enhancing the immunogenicity of a
CC peptide, where the peptide contains a class I epitope. The invention
CC includes methods for preparing peptides containing epitopes which have
CC enhanced ability to effect an immune response (compared to wild-type
CC epitopes). The peptides are referred to as heteroclitic analogues. The
CC method is useful for eliciting an immune response by contacting CTLs with
CC the immunogenically enhanced peptide in vitro in the presence of an
CC antigen presenting cell, or by administering to a subject a nucleic acid
CC molecule comprising a nucleotide sequence encoding the peptide. The
CC peptides are useful as reagents to evaluate an immune response and the
CC efficacy of the vaccine, and for making antibodies. The heteroclitic
CC analogues are useful in immunological compositions for the treatment of
CC viral diseases, cancer, and other conditions which are characterised by
CC displayed antigens on target cells. The present sequence represents a
CC class I epitope which may be used in the method of the invention
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPPAYRPPNAPIL 13
DB 1 TPPAYRPPNAPIL 13
RESULT 10
AAB82775
ID AAB82775 standard; protein; 13 AA.
XX
AC AAB82775;
XX
DT 06-AUG-2003 (revised)
DT 29-OCT-2001 (first entry)

XX Hepatitis B core antigen peptide.
DE
XX
KW Telomerase reverse transcriptase; hTERT; human; cytotoxic T lymphocyte;
KW major histocompatibility complex; cancer; tumour;
KW human leucocyte antigen; HLA-A2.1; HBVc; vaccine.
XX
OS Hepatitis B virus.
XX
PN WO200160391-A1.
XX
PD 23-AUG-2001.
XX
PF 15-FEB-2001; 2001WO-US005143.
XX
PR 15-FEB-2000; 2000US-0182685P.
XX
PR 15-FEB-2001; 2001US-00182685.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zanetti M;
XX
XX WPI; 2001-536552/59.
XX
XX Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,
PT for treating cancers or tumors or for inducing immune response against
PT tumors, comprises a telomerase reverse transcriptase peptide.
XX
XX Example 1; Page 12; 52pp; English.
XX
CC The present sequence is that of a hepatitis B virus core antigen (HBVc)
CC peptide comprising amino acid residues 128-140. The peptide was used to
CC immunise HHD mice and results were compared with those obtained using
CC human telomerase reverse transcriptase (hTERT) HLA-A2.1+ restricted
CC peptide p540 (see AAB82772). The induction of CTL responses in vitro and
CC in vivo, and the susceptibility to lysis of tumour cells of various
CC origins by hTERT CTL suggest that hTERT could serve as a universal cancer
CC vaccine for humans. A claimed universal vaccine for treating tumours of
CC any origin comprises at least 1 hTERT peptide. The peptide is 7-15 amino
CC acid residues in length and may be modified to enhance binding to the
CC major histocompatibility complex. Also claimed is a method for inducing
CC and enhancing a CTL response against cancer cells, involving harvesting
CC blood leucocytes, pulsing with hTERT, and contacting cancer cells with the
CC pulsed leucocytes. A method for targeting CTL to tumour cells is also
CC claimed, and involves administering a hTERT peptide to a mammal,
CC especially a cancer patient. (Updated on 06-AUG-2003 to correct OS
XX field.)
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPPAYRPPNAPIL 13
DB 1 TPPAYRPPNAPIL 13
RESULT 11
AAU00614
ID AAU00614 standard; peptide; 13 AA.
XX
AC AAU00614;
XX
DT 12-SEP-2001 (first entry)
XX
DE H-2 I-Ab-restricted HBV core antigen-derived T helper epitope.
XX
KW Human; MUC1; antigenic peptide; major histocompatibility complex; MHC-I;
KW glycoprotein; cytotoxic T lymphocytes; T cell response; cancer; vaccine;
KW cancer gene therapy; diagnosis; treatment; inflammatory disorder; HBV;
KW organ transplant rejection; graft versus host disease.

XX OS Hepatitis B virus.
 XX PN WO200118035-A2.
 XX PD 15-MAR-2001.
 XX PF 07-SEP-2000; 2000WO-EP008761.
 XX PR 08-SEP-1999; 99GB-00021242.
 XX PR 10-SEP-1999; 99EP-00402237.
 XX PR 03-MAR-2000; 2000US-0187215P.
 XX PA (TRGE) TRANSGENE SA.
 XX PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX PI Taylor-Papadimitriou J, Heukamp LC, Offringa R, Mellief CJM;
 XX PI Acres B, Thomas M;
 XX DR WPI; 2001-235187/24.
 XX PS New antigenic polypeptides of MUC-1 protein which activate cytotoxic T
 XX PT lymphocyte proteins and their analogs, useful for identifying a major
 XX PT histocompatibility complex class I restricted T cell response and for
 XX PT diagnosing cancer.
 XX PS Example 5; Page 42; 81pp; English.
 XX CC The sequence represents an H-2 I-Ab-restricted hepatitis B virus (HBV)
 XX CC core antigen-derived T helper epitope used in testing of human MUC1
 XX CC polypeptide derivatives through a cytotoxic T lymphocyte (CTL) assay.
 XX CC Derivative antigenic peptides of MUC1 protein bind at least one major
 XX CC histocompatibility complex class I (MHC-I) glycoprotein, which activates
 XX CC cytotoxic T lymphocytes to induce a protective response against tumours.
 XX CC Diagnosis of cancer involves determining the presence or absence in a
 XX CC host cell of MHC class I restricted-T cell response to a MUC1 derivative,
 XX CC where the presence of the MHC class I restricted T cell response
 XX CC indicates that the host has cancer. Measurement of the level of MHC class
 XX CC I restricted T cell response is also useful to monitor the severity of
 XX CC cancer, a larger response indicating a more severe cancer. MUC1
 XX CC derivatives are useful in cancer therapy and to follow MUC1 specific
 XX CC immune responses in patients during the course of disease and/or
 XX CC treatment. MUC1 DNA is useful in cancer gene therapy, vaccination and
 XX CC diagnosis. Compositions of the sequences are used in vaccines and
 XX CC treatments against cancer or diseases caused by an immune response, such
 XX CC as an inflammatory disorder, organ transplant rejection or graft versus
 XX CC host disease
 XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNPAPIL 13
 DB 1 TPPAYRPPNPAPIL 13
 RESULT 12
 AAU70851
 ID AAU70851 standard; peptide; 13 AA.
 AC AAU70851;
 XX 14-FEB-2002 (first entry)
 DE Hepatitis B virus antigen binding partner #83.
 XX Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;
 KW antiinflammatory; HBV core antigen; HBCAg; HBV E antigen; HBeAg;
 KW B cell mediated processing; T cell proliferation; cytokine production;
 KW immune system response.

XX OS Synthetic.
 XX PN WO200181421-A2.
 XX PD 01-NOV-2001.
 XX PF 20-APR-2001; 2001WO-IB000844.
 XX PR 21-APR-2000; 2000US-00356605.
 XX PA (TRIP-) TRIPEP AB.
 XX PI Sallberg M;
 XX DR WPI; 2002-055347/07.
 XX PT Novel peptide that binds to hepatitis B virus core or E antigen, useful
 XX PT for treating and preventing hepatitis B virus infection.
 XX PS Example 6; Page 28; 82pp; English.
 XX CC The invention relates to an isolated or purified peptide (I) which binds
 XX CC Hepatitis B virus (HBV) core antigen (HBCAg) or HBV E antigen (HBeAg).
 XX CC (I) is useful for treating or preventing Hepatitis B virus (HBV)
 XX CC infection, by identifying a subject in need of a molecule that inhibits
 XX CC HBV infection, and providing the subject with (I). (I) is also useful for
 XX CC determining the presence of HBV in a biological sample, and for
 XX CC inhibiting B cell mediated processing and uptake of HBCAg and/or HBeAg,
 XX CC by determining whether (I) inhibits B cell mediated processing and uptake
 XX CC of HBCAg and/or HBeAg by performing an assay of T cell proliferation or
 XX CC cytokine production. (I) is also useful for modulating an immune system
 XX CC response. (I) is useful as a template for a design of synthetic molecules
 XX CC including peptides, derivatives or modified peptides, peptidomimetics and
 XX CC chemicals. (I) is also useful as biotechnological tool, diagnostic
 XX CC reagent and as active ingredient in pharmaceuticals. (I) is also useful
 XX CC as detection reagents in conventional immunochemical techniques, as
 XX CC diagnostic reagents to detect HBV in biological sample, and to determine
 XX CC the efficacy of an HBV treatment protocol by monitoring the levels of
 XX CC HBCAg and/or HBeAg during and after treatment. AAU70766-AAU70876
 XX CC represent Hepatitis B virus (HBV) core antigen (HBCAg) or HBV E antigen
 XX CC (HBeAg) binding partners as described in the invention
 XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNPAPIL 13
 DB 1 TPPAYRPPNPAPIL 13
 RESULT 13
 ABB76787
 ID ABB76787 standard; peptide; 13 AA.
 XX ABB76787;
 XX 31-MAY-2002 (first entry)
 DT HBV peptide 128-140.
 DE Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;
 KW human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.
 XX Unidentified.
 XX FR2812087-A1.
 XX 25-JAN-2002.
 XX

PF 21-JUL-2000; 2000FR-00009591.
 XX
 PR 21-JUL-2000; 2000FR-00009591.
 XX
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Komatopoulos K, Tourdot S, Scardino A, Gross DA;
 XX
 XX WPI; 2002-189946/25.
 XX
 DR Identifying subdominant or cryptic epitopes, useful in immunotherapy of
 PT cancer and viral infection, comprises testing modified, non-immunogenic
 PT peptides for induction of cytotoxic T cells.
 XX
 XX Example 1; Page 14; 62pp; French.
 XX
 XX The present invention relates to subdominant/cryptic epitopes that are
 CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The
 CC epitopes or chimeric polypeptides containing them and nucleic acid
 CC encoding them are useful for preventative or curative immunotherapy of
 CC cancer and viral infections, particularly where used as vaccines. The
 CC present peptide was used to illustrate the invention
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 100.0%; Score 74; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TPPAYRPPNAPIL 13
 Db 1 TPPAYRPPNAPIL 13
 RESULT 14
 ID ABG62860 standard; peptide; 13 AA.
 AC ABG62860;
 XX
 XX 21-AUG-2002 (first entry)
 XX
 DE Antigenic domain peptide from a Hepatitis B virus protein.
 XX
 DE Ligand/receptor specificity exchanger; antibody; pathogen receptor;
 KW bacterial infection; viral infection; yeast infection; cancer;
 KW parasitic infection; fungal infection; proliferation; antibacterial;
 KW virucide; cytostatic; antifungal; antigenic domain.
 XX
 OS Hepatitis B virus.
 XX
 XX WO200224887-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 19-SEP-2001; 2001WO-IB002327.
 XX
 XX 19-SEP-2000; 2000US-00664025.
 XX
 XX (TRIP-) TRIPEP AB.
 XX
 XX Sallberg M, Flock J;
 XX
 DR WPI; 2002-489707/52.
 XX
 XX Novel ligand/receptor specificity exchanger that redirects antibodies to
 PT receptors on pathogen or tumor cell, has specificity domain having ligand
 PT for receptor, and antigenic domain having epitope of pathogen or toxin.
 XX
 XX Claim 14; Page 14; 79pp; English.
 XX
 XX The present invention relates to ligand/receptor specificity exchangers
 CC comprising at least one specificity domain comprising a ligand for a

CC receptor, and at least one antigenic domain joined to the specificity
 CC domain, where the antigenic domain comprises an epitope of a pathogen or
 CC toxin. The ligand/receptor specificity exchangers redirect antibodies to
 CC receptors present on pathogens. They are useful for preventing and
 CC treating human diseases such as bacterial, viral, yeast, parasitic and
 CC fungal infections, and cancer. These compositions act by inhibiting
 CC proliferation of pathogens, or cancer cells. One of the prophylactic
 CC applications of the ligand/receptor specificity exchangers includes
 CC coating or crosslinking it to a medical device or implant which include
 CC implantable medical devices that tend to serve as foci for infection by a
 CC number of bacterial species. ABG62853-ABG62869 represent antigenic domain
 CC peptides used in the methods of the present invention
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 100.0%; Score 74; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TPPAYRPPNAPIL 13
 Db 1 TPPAYRPPNAPIL 13
 RESULT 15
 ABP52344
 ID ABP52344 standard; peptide; 13 AA.
 XX
 AC ABP52344;
 XX
 XX 17-OCT-2002 (first entry)
 DT
 XX
 DE TH epitope.
 XX
 KW Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;
 KW tumour; immune response; cancer; vaccine; antibody.
 XX
 OS Synthetic.
 XX
 PN WO200258728-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 28-JAN-2002; 2002WO-GB000354.
 XX
 PR 26-JAN-2001; 2001GB-00002145.
 XX
 XX (SCAN-) SCANCELL LTD.
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 XX Durrant LG, Parsons T, Robins A;
 XX
 XX WPI; 2002-608418/65.
 XX
 XX Use of polypeptides and nucleic acids encoding the polypeptides, in
 PT manufacturing medicament for stimulating a cytotoxic T cell response and
 PT for preventing or treating cancer, e.g. colorectal, lung, breast or
 PT ovarian cancer.
 XX
 XX Example 11; Page 45; 87pp; English.
 XX
 XX The present invention describes the use of a polypeptide (I) in the
 CC manufacture of a medicament for stimulating a cytotoxic T cell response,
 CC where (I) comprises a first portion comprising the part of human Fc that
 CC binds to CD64 and a second portion comprising one or more heterologous T
 CC cell epitopes. Also described is a method of stimulating a cytotoxic T
 CC cell response in a patient such as a mammal, preferably human, by
 CC administering (I) to the patient. (I) has cytostatic activity and can be
 CC used in vaccine production. (I) and the nucleic acid encoding (I) are
 CC useful in the manufacture of a medicament for stimulating cytotoxic T
 CC cell response. The medicament is useful for preventing and/or treating
 CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The
 CC medicament stimulates cytotoxic and helper T cell responses. The

CC antibodies are useful as vaccines to stimulate helper and cytotoxic T
CC cell responses. The polypeptides and nucleic acids are useful in
CC optimising immunisation schedules for enhancing a protective immune
CC response against cancer. The present sequence represents a TH epitope
CC which is used in an example from the present invention

XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
| | | | | | | | | | | | |
Db 1 TPPAYRPPNAPIL 13

Search completed: August 9, 2004, 18:34:34
Job time : 51 secs

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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:33:55 ; Search time 18 Seconds
(without alignments)
37.285 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPAYRPNAPIL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 127817

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	13	1	US-08-305-871A-14
2	74	100.0	13	4	US-08-464-496-19
3	74	100.0	13	4	US-08-788-822A-16
4	74	100.0	13	4	US-08-197-484-113
5	74	100.0	13	4	US-09-311-784A-49
6	74	100.0	13	4	US-09-664-945-50
7	74	100.0	13	5	PCT-US92-07218-19
8	74	100.0	13	5	PCT-US95-02121-113
9	74	100.0	13	5	PCT-US95-16415-9
10	55	74.3	10	3	US-08-159-339A-402
11	51	68.9	9	3	US-08-159-339A-393
12	51	68.9	9	4	US-09-311-784A-198
13	45	60.8	12	3	US-08-602-999A-268
14	45	60.8	12	4	US-09-500-124-268
15	44	59.5	10	2	US-08-737-085A-7
16	44	59.5	10	3	US-09-246-258-7
17	44	59.5	10	3	US-09-532-106-7
18	44	59.5	10	4	US-09-839-666-7
19	42	56.8	13	2	US-08-737-085A-20
20	42	56.8	13	3	US-09-246-258-20
21	42	56.8	13	3	US-09-532-106-20
22	42	56.8	13	4	US-08-839-666-20
23	39	52.7	8	2	US-08-737-085A-6
24	39	52.7	8	3	US-09-246-258-6
25	39	52.7	8	3	US-09-532-106-6
26	39	52.7	8	4	US-09-839-666-6
27	38	51.4	11	1	US-08-336-343A-26

28 38 51.4 11 3 US-08-652-877-23 Sequence 23, Appl
29 38 51.4 11 3 US-08-476-515A-23 Sequence 23, Appl
30 38 51.4 12 4 US-09-845-917A-22 Sequence 22, Appl
31 37 50.0 10 1 US-08-477-509B-11 Sequence 11, Appl
32 37 50.0 10 3 US-08-482-085B-11 Sequence 11, Appl
33 37 50.0 10 4 US-09-444-791A-11 Sequence 11, Appl
34 37 50.0 12 4 US-09-428-082B-313 Sequence 313, Appl
35 36 48.6 12 2 US-08-459-568-61 Sequence 61, Appl
36 36 48.6 12 3 US-08-399-411-61 Sequence 61, Appl
37 36 48.6 12 3 US-08-516-859A-61 Sequence 61, Appl
38 36 48.6 12 3 US-09-078-173A-22 Sequence 22, Appl
39 36 48.6 12 4 US-09-586-472-61 Sequence 61, Appl
40 36 48.6 12 4 US-09-528-706-61 Sequence 61, Appl
41 36 48.6 12 4 US-09-428-082B-312 Sequence 312, Appl
42 36 48.6 13 3 US-09-078-173A-23 Sequence 23, Appl
43 35 47.3 10 1 US-08-230-047-11 Sequence 11, Appl
44 35 47.3 11 4 US-09-311-784A-181 Sequence 181, Appl
45 34 45.9 10 3 US-08-602-999A-141 Sequence 141, Appl

ALIGNMENTS

RESULT 1
US-08-305-871A-14
; Sequence 14, Application US/08305871A
; Patent No. 5736142
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Grey, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffrey L.
; TITLE OF INVENTION: Alteration of Immune Response Using Pan
; TITLE OF INVENTION: DR-Binding Peptides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,871A
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,101
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-0062-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-305-871A-14

Query Match 100.0%; Score 74; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
|||||
Db 1 TPPAYRPPNAPIL 13

RESULT 2

US-08-464-496-19
; Sequence 19, Application US/08464496
; Patent No. 6322789
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: Vitello, Maria
; APPLICANT: Chesnut, Robert
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; FILE REFERENCE: 39963-20001.13
; CURRENT APPLICATION NUMBER: US/08/464,496
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 07/935,811
; PRIOR FILING DATE: 1992-08-26
; PRIOR APPLICATION NUMBER: 07/874,491
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/827,682
; PRIOR FILING DATE: 1992-01-29
; PRIOR APPLICATION NUMBER: 07/749,568
; PRIOR FILING DATE: 1991-08-26
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T helper epitope HBC 128-140
US-08-464-496-19

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
|||||
Db 1 TPPAYRPPNAPIL 13

RESULT 3

US-08-788-822A-16
; Sequence 16, Application US/08788822A
; Patent No. 6413935
; GENERAL INFORMATION:
; APPLICANT: Alexander, Jeffrey L.
; APPLICANT: Deftrees, Shawn
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Induction of Immune Response Against
Desired Determinants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,822A
; FILING DATE: 23-JAN-1997

CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,510
; FILING DATE: 24-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 014137-009210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-788-822A-16

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
|||||
Db 1 TPPAYRPPNAPIL 13

RESULT 4

US-08-197-484-113
; Sequence 113, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CYT IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990

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; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-113

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
Db 1 TTPAYRPPNAPIL 13

RESULT 5
US-09-311-784A-49
; Sequence 49, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39563-20022.01
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US/09/311,784A
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-09-311-784A-49

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
Db 1 TTPAYRPPNAPIL 13

RESULT 6
US-09-664-945-50
; Sequence 50, Application US/09664945
; Patent No. 6660842
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
; FILE REFERENCE: TRIPP.007CP3
; CURRENT APPLICATION NUMBER: US/09/664,945
; CURRENT FILING DATE: 2000-03-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
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; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: SE 9401460
; PRIOR FILING DATE: 1994-04-28
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antigenic domain peptide
US-09-664-945-50

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
Db 1 TTPAYRPPNAPIL 13

RESULT 7
PCT-US92-07218-19
; Sequence 19, Application PC/TUS9207218
; GENERAL INFORMATION:
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Chesnut, Robert W.
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07218
; FILING DATE: 19920826
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-26-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 402:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-402

Query Match 74.3%; Score 55; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AYRPPNAPIL 13
DB 1 AYRPPNAPIL 10

RESULT 11
US-08-159-339A-393
; Sequence 393, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cells, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-393

Query Match 68.9%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AYRPPNAPI 12
DB 1 AYRPPNAPI 9

RESULT 12
US-09-311-784A-198
; Sequence 198, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 198
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV NUC 131 (peptide 1090.02)
; US-09-311-784A-198

Query Match 68.9%; Score 51; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AYRPPNAPI 12
DB 1 AYRPPNAPI 9

RESULT 13
US-08-602-999A-268
; Sequence 268, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
```

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; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 268:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-268

Query Match 60.8%; Score 45; DB 3; Length 12;
Best Local Similarity 63.6%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPAYRPPNAPI 12
   |||||
Db 2 PPAYPPPPVPV 12

RESULT 14
US-09-500-124-268
; Sequence 268, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:

Query Match 60.8%; Score 45; DB 3; Length 12;
Best Local Similarity 63.6%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPAYRPPNAPI 12
   |||||
Db 2 PPAYPPPPVPV 12

RESULT 15
US-08-737-085A-7
; Sequence 7, Application US/08737085A
; Patent No. 5869232
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,085A
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/0C569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEX: 212-753-6237
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-737-085A-7

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Query Match 59.5%; Score 44; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. NO. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 RPPNAPIL 13
Db 1 RPPNAPIL 8

Search completed: August 9, 2004, 18:36:38
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:35:46 ; Search time 40 Seconds
(without alignments)
101.947 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 31362936 residues

Total number of hits satisfying chosen parameters: 189912

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	13	9	US-09-839-447A-86
2	74	100.0	13	10	US-09-277-074-9
3	74	100.0	13	12	US-09-277-064-9
4	74	100.0	13	12	US-10-371-525-49
5	74	100.0	13	12	US-10-372-735-55
6	74	100.0	13	12	US-10-182-252A-1374
7	74	100.0	13	12	US-10-333-430-63
8	74	100.0	13	12	US-09-788-110A-4
9	74	100.0	13	12	US-09-055-744-10
10	74	100.0	13	13	US-10-106-487-22
11	74	100.0	13	14	US-10-128-711-113
12	74	100.0	13	14	US-10-116-118-30
13	74	100.0	13	15	US-10-371-069-49
14	74	100.0	13	15	US-10-371-645-43
15	74	100.0	13	15	US-10-371-260-49

Sequence 86, Appl
Sequence 22, Appl
Sequence 50, Appl
Sequence 600, Appl
Sequence 599, Appl
Sequence 613, Appl
Sequence 586, Appl
Sequence 587, Appl
Sequence 598, Appl
Sequence 612, Appl
Sequence 626, Appl
Sequence 585, Appl
Sequence 379, Appl
Sequence 584, Appl
Sequence 311, Appl
Sequence 370, Appl
Sequence 597, Appl
Sequence 611, Appl
Sequence 625, Appl
Sequence 639, Appl
Sequence 198, Appl
Sequence 198, Appl
Sequence 198, Appl
Sequence 198, Appl
Sequence 198, Appl
Sequence 596, Appl
Sequence 610, Appl
Sequence 624, Appl
Sequence 638, Appl
Sequence 651, Appl
Sequence 583, Appl

ALIGNMENTS

RESULT 1

US-09-839-447A-86

; Sequence 86, Application US/09839447A

; Patent No. US20020058247A1

; GENERAL INFORMATION:

; APPLICANT: Sallberg, Matti

; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE

; FILE REFERENCE: TRIPEP.020CPI

; CURRENT APPLICATION NUMBER: US/09/839,447A

; PRIOR FILING DATE: 2001-08-09

; PRIOR FILING DATE: 2000-04-21

; NUMBER OF SEQ ID NOS: 111

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 86

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificial Peptide

US-09-839-447A-86

Query Match 100.0%; Score 74; DB 9; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0022;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 1 TPPAYRPPNAPIL 13

RESULT 2

US-09-277-074-9

; Sequence 9, Application US/09277074

; Publication No. US2003002820A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Linda A.

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; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR21558
; CURRENT APPLICATION NUMBER: US/09/277,074
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
; OTHER INFORMATION: Artificially Synthesized Peptides
US-09-277-074-9

Query Match 100.0%; Score 74; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 3
US-09-277-064-9
; Sequence 9, Application US/09277064
; Publication No. US20030064916A1
; GENERAL INFORMATION:
; APPLICANT: Sherwin, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR21525
; CURRENT APPLICATION NUMBER: US/09/277,064
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
; OTHER INFORMATION: Artificially Synthesized Peptides
US-09-277-064-9

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 4
US-10-371-525-49.
; Sequence 49, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39563-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21

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; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-525-49

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 5
US-10-372-735-55
; Sequence 55, Application US/10372735
; Publication No. US20030225251A1
; GENERAL INFORMATION:
; APPLICANT: Salberg, Matti
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; FILE REFERENCE: TRIPEP.7AUC4CP1
; CURRENT APPLICATION NUMBER: US/10/372,735
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/234,579
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE95/00468
; PRIOR FILING DATE: 1995-04-27
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/664,025
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: PCT/IB01/02327
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 10/153,271
; PRIOR FILING DATE: 2002-05-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptides
US-10-372-735-55

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

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RESULT 6
US-10-182-252A-1374
; Sequence 1374, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PC/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1374
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-182-252A-1374

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 1 TPPAYRPPNAPIL 13

RESULT 7
US-10-333-430-63
; Sequence 63, Application US/10333430
; Publication No. US20040072240A1
; GENERAL INFORMATION:
; APPLICANT: INSERM
; APPLICANT: INSTITUT GUSTAVE ROUSSY
; APPLICANT: KOSMATOPOULOS, Kostas
; APPLICANT: TOURDOT, Sophie
; APPLICANT: SCARDINO, Antonio
; APPLICANT: GROSS, David, Alexandre
; TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
; TITLE OF INVENTION: IMMUNOTHERAPY
; FILE REFERENCE: 33339/259034
; CURRENT APPLICATION NUMBER: US/10/333,430
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: FR 0003591
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-333-430-63

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 1 TPPAYRPPNAPIL 13

RESULT 8
US-09-788-110A-4
; Sequence 4, Application US/09788110A
; Publication No. US20040086518A1
; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; TITLE OF INVENTION: Telomerase Reverse Transcriptase
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-110A-4

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 1 TPPAYRPPNAPIL 13

RESULT 9
US-09-055-744-10
; Sequence 10, Application US/09055744
; Publication No. US20010019714A1
; GENERAL INFORMATION:
; APPLICANT: Sia, Charles
; APPLICANT: Chong, Pele
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: HIV-SPECIFIC CYTOTONIX T-CELL RESPONSES
; FILE REFERENCE: 1038-746
; CURRENT APPLICATION NUMBER: US/09/055,744
; CURRENT FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-055-744-10

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 1 TPPAYRPPNAPIL 13

RESULT 10
US-10-106-487-22
; Sequence 22, Application US/10106487
; Publication No. US20020164721A1
; GENERAL INFORMATION:
; APPLICANT: FIRAT, HUSEYIN
; APPLICANT: LEMONNIER, FRANCOIS
; APPLICANT: LANGLADE-DEMOYEN, PIERRE
; APPLICANT: MICHEL, MARIE-LOUISE
; TITLE OF INVENTION: DESIGN OF A POLYPEPTIC CONSTRUCT FOR THE INDUCTION
; TITLE OF INVENTION: OF
; TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING
```

;; TITLE OF INVENTION: HHD MICE
;; FILE REFERENCE: 03495.0196 SEQUENCE LISTING
;; CURRENT APPLICATION NUMBER: US/10/106,487
;; CURRENT FILING DATE: 2002-03-27
;; PRIOR APPLICATION NUMBER: 09/675,673
;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: 60/158,356
;; PRIOR FILING DATE: 1999-10-12
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 22
;; LENGTH: 13
;; TYPE: PRT
;; ORGANISM: Hepatitis B virus
US-10-106-487-22

Query Match 100.0%; Score 74; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 11
US-10-128-711-113
; Sequence 113, Application US/10128711
; Publication No. US20030093634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 113:

;; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-128-711-113

Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 12
US-10-116-118-30
; Sequence 30, Application US/10116118
; Publication No. US20030143672A1
; GENERAL INFORMATION:
; APPLICANT: Targri, Shabnam
; APPLICANT: Sette, Alessandro
; APPLICANT: Fikes, John D.
; APPLICANT: Ishioka, Glenn
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.0090003
; CURRENT APPLICATION NUMBER: US/10/116,118
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/166,529
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: US 60/239,008
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: (HBV core)
US-10-116-118-30

Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 13
US-10-371-069-49
; Sequence 49, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; IMMUNE RESPONSE AND METHODS OF USING THE SAME
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904


```
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-069-49

Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TPPAYRPPNPAIL 13
Db      1 TPPAYRPPNPAIL 13
|||||
|||||

RESULT 14
US-10-371-645-49
; Sequence 49, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-645-49

Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TPPAYRPPNPAIL 13
Db      1 TPPAYRPPNPAIL 13
|||||
|||||

RESULT 15
US-10-371-260-49
; Sequence 49, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
```

```
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-260-49
```

```
Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TPPAYRPPNPAIL 13
Db      1 TPPAYRPPNPAIL 13
|||||
|||||

Search completed: August 9, 2004, 18:41:00
Job time : 40 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:31:10 ; Search time 16 Seconds
(without alignments)
78.156 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1827

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	39.2	11	1 XAVIBH	bradykinin-potenti
2	29	39.2	12	2 S71380	lebetin 1 isoform
3	29	39.2	13	2 S21152	tryptophyllin-rela
4	29	39.2	13	2 S09716	2S albumin large c
5	24	32.4	13	2 G37266	Ig heavy chain C r
6	23	31.1	9	2 A61358	bradykinin-like pe
7	23	31.1	9	2 A61057	Thr-6 bradykinin -
8	23	31.1	9	2 A26744	bradykinin-like pe
9	23	31.1	9	2 A61363	bradykinin - commo
10	23	31.1	9	2 A60579	bradykinin-like pe
11	23	31.1	9	2 B60246	ornitho-kinin - ch
12	23	31.1	9	2 S55433	bradykinin - horn
13	23	31.1	9	2 A43065	hydroxyproline-3-b
14	23	31.1	11	2 A61365	phyllokinin-Rohd
15	23	31.1	11	2 B26744	megascollakinin -
16	23	31.1	11	2 S13279	Ile-Ser-bradykinin
17	23	31.1	12	2 A61360	vespakinin M - hor
18	23	31.1	12	2 A61359	vespakinin X - hor
19	23	31.1	13	2 A61361	bradykinin-like pe
20	22	29.7	10	2 S39030	lysyl-bradykinin -
21	22	29.7	11	2 I33098	173K exantigen -
22	22	29.7	12	2 P00046	ATP synthase D cha
23	22	29.7	12	2 B39690	neural cell adhesi
24	22	29.7	13	2 D39690	neural cell adhesi
25	22	29.7	13	2 A05174	tryptophyllin-13 -
26	21	28.4	7	2 A61081	tryptophyllin, bas
27	21	28.4	10	2 S26506	collagen alpha 1(V
28	20	27.0	8	2 B39745	endoglycosylcerami
29	20	27.0	9	2 P40139	carbon-monoxide de

ALIGNMENTS

RESULT 1

XAVIBH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994

C;Accession: J00002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese

A;Reference number: J00002; PMID:86177022; PMID:3008123

A;Accession: J00002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyrog

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 39.2%; Score 29; DB 1; Length 11;

Best Local Similarity 71.4%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 RPPNAPI 12

DB 3 RPPGPPI 9

RESULT 2

S71380

lebetin 1 isoform beta - Vipera lebetina

C;Species: Vipera lebetina

C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999

C;Accession: S71380

R;Barbouche, R.; Marrakchi, N.; Mansuelle, P.; Krifi, M.; Ferouillet, E.; Rochat, H.; El

PEBS Lett 392, 6-10, 1996

A;Title: Novel anti-platelet aggregation polypeptides from Vipera lebetina venom: isolat

A;Reference number: S71379; PMID:96354866; PMID:8769304

A;Accession: S71380

A;Molecule type: protein

A;Residues: 1-12 <BAR>

A;Experimental source: venom

C;Keywords: anticoagulant; venom

Query Match 39.2%; Score 29; DB 2; Length 12;

Best Local Similarity 62.5%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPAYRPPN 9

DB 4 PPKKGPPN 11

```

RESULT 3
S21152
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S21152
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Palconieri Erspaner, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of th
A:Reference number: S21152; MUID:92339502; PMID:1633846
A:Accession: S21152
A:Molecule type: protein
A:Residues: 1-13 <MIG>
A:Experimental source: skin
C:Superfamily: unassigned animal peptides

Query Match 39.2%; Score 29; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PAYRPPNAPI 12
DB 4 PFYPPPIYPV 13

RESULT 4
S09716
2S albumin large chain (1 and 2) nII - rape (fragments)
N:Alternate names: 2S albumin large chain nIII
C:Species: Brassica napus (rape)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C:Accession: S09716; S09718; S09717
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09716
A:Molecule type: protein
A:Residues: 1-9;10-13 <MON>
A:Experimental source: seed
A:Note: 3-Ser was also found
A:Accession: S09718
A:Molecule type: protein
A:Residues: 1-9;10-13 <MO2>
A:Experimental source: seed
A:Accession: S09717
A:Molecule type: protein
A:Residues: 1-9;10-13 <MO3>
A:Experimental source: seed

Query Match 39.2%; Score 29; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PAYRPPNAP 11
DB 4 PQRRPPPGP 12

RESULT 5
G37266
Ig heavy chain C region (Py2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: G37266
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 265, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: G37266
A>Status: preliminary
A:Molecule type: mRNA

```

A;Residues: 1-13 <RUF>

Query Match 32.4%; Score 24; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 8.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPPAYRP 7
DB 4 TPSPQYP 10

RESULT 6

A61358
bradykinin-like peptide I - Japanese pond frog
C:Species: Rana nigromaculata (Japanese pond frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C:Accession: A61358
R:Nakajima, T.
Chem. Pharm. Bull. 16, 769-770, 1968
A:Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin
A:Reference number: A61358; MUID:68412013; PMID:5677638
A:Accession: A61358
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: unassigned animal peptides
C:Keywords: skin

Query Match 31.1%; Score 23; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
DB 2 PGFTFP 7

RESULT 7

A61057
Thr-6 bradykinin - scoliid wasp (Colpa interrupta)
C:Species: Colpa interrupta
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Aug-2000
C:Accession: A61057
R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.
Comp. Biochem. Physiol. C 96, 157-162, 1990
A:Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynapt
A:Reference number: A61057; MUID:91130217; PMID:1980872
A:Accession: A61057
A:Molecule type: protein
A:Residues: 1-9 <PIB>
C:Superfamily: unassigned animal peptides
C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 31.1%; Score 23; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
DB 2 PGFTFP 7

RESULT 8

A26744
bradykinin-like peptide - garden dagger wasp
N:Alternate names: Thr-6-bradykinin
C:Species: Megascollia flavifrons (garden dagger wasp)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000
C:Accession: A26744
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
Toxicol 25, 527-535, 1987
A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp
A:Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: A26744
 A;Molecule type: protein
 A;Residues: 1-9 <YAS>
 C;Superfamily: unassigned animal peptides

Query Match 31.1%; Score 23; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
 ||:|
 Db 2 PPGFTP 7

RESULT 9

A61363
 bradykinin - common frog
 C;Species: Rana temporaria (common frog)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
 C;Accession: A61363
 R;Anastasi, A.; Erspamer, V.; Bertaccini, G.
 Comp. Biochem. Physiol. A 14, 43-52, 1965
 A;Title: Occurrence of bradykinin in the skin of Rana temporaria.
 A;Reference number: A61363
 A;Accession: A61363
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <ANA>
 C;Superfamily: unassigned animal peptides
 C;Keywords: skin

Query Match 31.1%; Score 23; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
 ||:|
 Db 2 PPGFTP 7

RESULT 10

A60579
 bradykinin-like peptide - slider turtle
 C;Species: Pseudemys scripta (slider)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C;Accession: A60579
 R;Conlon, J.M.; Hicks, J.W.; Smith, D.D.
 Endocrinology 126, 985-991, 1990
 A;Title: Isolation and biological activity of a novel kinin ([Thr(6)]bradykinin) from the
 C;Reference number: A60579; PMID:2298179
 A;Accession: A60579
 A;Molecule type: protein
 A;Residues: 1-9 <CON>
 C;Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammalian
 C;Superfamily: unassigned animal peptides
 C;Keywords: plasma

Query Match 31.1%; Score 23; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
 ||:|
 Db 2 PPGFTP 7

RESULT 11

B60246
 ornitho-kinin - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 18-Aug-2000
 C;Accession: B60246
 R;Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.

Adv. Exp. Med. Biol. 247A, 359-367, 1989
 A;Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemical
 A;Reference number: A60246; PMID:90102072; PMID:2603803
 A;Accession: B60246
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <KIM>
 C;Superfamily: unassigned animal peptides

Query Match 31.1%; Score 23; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
 ||:|
 Db 2 PPGFTP 7

RESULT 12

S65433
 bradykinin - horn fly (fragment)
 C;Species: Haematobia irritans (horn fly)
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C;Accession: S65433
 R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P.
 Eur. J. Biochem. 237, 414-423, 1996
 A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran
 A;Reference number: S65431; PMID:96215437; PMID:8647080
 A;Accession: S65433
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <WIJ>
 A;Note: the source is designated as Haematobia irritans exigua

Query Match 31.1%; Score 23; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
 ||:|
 Db 2 PPGFTP 7

RESULT 13

A43065
 hydroxyproline-3-bradykinin - frog (Helleophryne purcelli)
 C;Species: Helleophryne purcelli
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
 C;Accession: A43065
 R;Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.
 Experientia 35, 1133, 1979
 A;Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South A
 A;Reference number: A43065; PMID:80024576; PMID:488255
 A;Accession: A43065
 A;Molecule type: protein
 A;Residues: 1-9 <NAK>
 C;Keywords: bradykinin; hydroxyproline; skin
 F;3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 31.1%; Score 23; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
 ||:|
 Db 2 PPGFTP 7

RESULT 14

A61365
 phyllokinin - Rohde's leaf frog
 N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C/Accession: A61365
R/Anastasi, A.; Bertaccini, G.; Erspamer, V.
Br. J. Pharmacol. 27, 479-485, 1966
A/Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate)
A/Reference number: A61365; MUID:67179312; PMID:5970899

A/Accession: A61365
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-11 <ANA>
C/Superfamily: unassigned animal peptides
C/Keywords: sulfoprotein
F/11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 31.1%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
|||.||
Db 2 PPGFSP 7

RESULT 15

B26744
megascaliakinin - garden dagger wasp
N/Alternate names: 6-Thr-bradykinin-Lys-Ala
C/Species: Megascalia flavifrons (garden dagger wasp)
C/Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000
C/Accession: B26744; A28609
R/Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
Toxicol. 25, 527-535, 1987
A/Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp
A/Reference number: A94322; MUID:87293024; PMID:3617088
A/Accession: B26744
A/Molecule type: protein
A/Residues: 1-11 <YAS>
R/Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.
Toxicol. 26, 34, 1988
A/Title: Two kinins isolated from the venom of Megascalia flavifrons.
A/Reference number: A28609
A/Accession: A28609
A/Molecule type: protein
A/Residues: 1-11 <NAK>
C/Superfamily: unassigned animal peptides
C/Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 31.1%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
|||.||
Db 2 PPGFSP 7

Search completed: August 9, 2004, 18:36:09
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:29:25 ; Search time 13 Seconds
(without alignments)
52.070 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74
Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 597

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29	39.2	11	1 BPP_AGKHP	P04562 agkistrodon
2	24	32.4	7	1 TPFF_PACDA	P83455 pachymedusa
3	23	31.1	8	1 PKP2_PERAM	P82692 periplaneta
4	23	31.1	9	1 KNL3_BOMVA	P83058 bombina var
5	23	31.1	11	1 BSK_MEGFL	P12797 megascalia
6	23	31.1	12	1 GRAR_RANRU	P40754 rana rugosa
7	23	31.1	13	1 BRK_PARID	P42717 parapolybia
8	22	29.7	10	1 BRK_ONCMY	Q9PZ1 oncothynchu
9	22	29.7	13	1 TV13_PHYRO	P04096 phyllomedus
10	20	27.0	6	1 OVM_LBPDE	P42985 leptinotars
11	20	27.0	10	1 TMOF_AEDAB	P19425 aedes aegypt
12	19	25.7	9	1 NEUU_CAVPO	P34966 cavia porce
13	19	25.7	10	1 BPP8_BOTIN	P30426 bothrops in
14	19	25.7	10	1 URE3_MORMO	P17339 morganelia
15	19	25.7	12	1 FARI_CALVO	P41869 calliphora
16	19	25.7	12	1 TAL0_TREME	P01371 tremella me
17	18	24.3	12	1 FAR7_PENMO	P83322 penaeus mon
18	18	24.3	13	1 BLAC_STRGR	P81173 streptomyc
19	17	23.0	7	1 MNP1_LEPDE	P42984 leptinotars
20	17	23.0	7	1 UF04_MOUSE	P38642 mus musculu
21	17	23.0	9	1 ISOT_CYPCA	P42993 cyprinus ca
22	17	23.0	9	1 OXYT_OCTVU	P80027 octopus vul
23	17	23.0	11	1 BPP3_BOTIN	P30423 bothrops in
24	17	23.0	11	1 BPP4_BOTIN	P30423 bothrops in
25	17	23.0	11	1 BPPB_AGKHA	P01021 agkistrodon
26	17	23.0	11	1 TKM1_UPEIN	P82026 uperoleia i
27	17	23.0	11	1 TKM1_UPERU	P08612 uperoleia i
28	17	23.0	13	1 ADFE_TENMO	P83109 tenebrio mo
29	16	21.6	9	1 OXYA_SCYCA	P42996 scylliorhinu
30	16	21.6	9	1 OXYF_SCYCA	P42997 scylliorhinu
31	16	21.6	9	1 OXYV_SQUAC	P43000 squalus aca
32	16	21.6	10	1 ESTA_SCHGA	P81012 schizaphis
33	16	21.6	10	1 LPK2_LOCMI	P41488 locusta mig

P81532 microplitis
P83277 macrobrachi
P82618 periplaneta
P29177 bos taurus
P43999; squalus aca
P32878 oryctolagus
P29261 prunus sero
P80336 oryctolagus
P80337 ovis aries
P83278 macrobrachi
P30088 homo sapien
P22790 achatina fu

34 16 21.6 13 1 MPI_MICOC
35 15 20.3 8 1 FAR4_MACRS
36 15 20.3 8 1 PPK3_PERAM
37 15 20.3 9 1 MGMT_BOVIN
38 15 20.3 9 1 OXVA_SQUAC
39 15 20.3 9 1 OXYT_RABIT
40 15 20.3 10 1 AH3_FRUSE
41 15 20.3 10 1 COXQ_RABIT
42 15 20.3 10 1 COXQ_SHEEP
43 15 20.3 10 1 FAR5_MACRS
44 15 20.3 10 1 UPA2_HUMAN
45 15 20.3 11 1 CEP1_ACHFUFU

ALIGNMENTS

RESULT 1
BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562; 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -/- FUNCTION: This peptide both inhibits the activity of the
angiotensin-converting enzyme and enhances the action of
bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;
Query Match 39.2%; Score 29; DB 1; Length 11;
Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 RPPNAPI 12
Db 3 RPPGPPI 9
RESULT 2
TPFF_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (pdt-1).
OS Pachymedusa dactylosa (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF

RP PRO-7.
 RC TISSUE=Skin secretion;
 RA Chen T.B., Orr D.F., Shaw C.;
 RT "Pachymedusa danielcolor tryptophyllin-1 (Pdt-1): structural
 RT characterization, pharmacological activity and cloning of precursor
 RT cDNA";
 RL Submitted (SEP-2002) to Swiss-Prot.
 CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
 CC smooth muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
 KW Amphibian defense peptide; Amidation; Hydroxylation.
 FT MOD_RES 3
 FT MOD_RES 3 HYDROXYLATION.
 FT MOD_RES 7
 FT MOD_RES 7 AMIDATION.
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;
 Query Match 32.4%; Score 24; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PPAVRP 7
 DB 2 PPAWVP 7
 RESULT 3
 ID PKK2_PPRAM STANDARD; PRT; 8 AA.
 AC P82692;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=97353923; PubMed=9210163;
 RA Predel R., Keilner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT retrocerebral complex of the American cockroach.";
 RL Peptides 18:473-478 (1997).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363 (2000).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 8
 FT MOD_RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;
 Query Match 31.1%; Score 23; DB 1; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.4e+05;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 PPNAPIL 13
 ||| |

Db 2 PPFAPRL 8
 RESULT 4
 ID KNL3_BOMVA STANDARD; PRT; 9 AA.
 AC P83058;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE [Thr6]bradykinin.
 OS Bombina variegata (Yellow-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OX NCBI_TaxID=8348;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Skin secretion;
 RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
 RT "Cloning and post-translational processing of frog skin kininogens.";
 RL Submitted (JUL-2001) to Swiss-Prot.
 CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
 CC arterial smooth muscle and constriction of intestinal smooth
 CC muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 KW Amphibian defense peptide; Vasodilator; Bradykinin.
 SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;
 Query Match 31.1%; Score 23; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PPAVRP 7
 DB 2 PPGTTP 7
 RESULT 5
 ID BRK_MEGFL STANDARD; PRT; 11 AA.
 AC P12797;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
 DE peptide ([Thr6]bradykinin)].
 OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Scolidae; Megascolia.
 OX NCBI_TaxID=7437;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 RT solitary wasp Megascolia flavifrons.";
 RL Toxicon 25:527-535 (1987).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Nakajima T., Piek T., Yasuhara T., Mantel P.;
 RT "Two kinins isolated from the venom of Megascolia flavifrons.";
 RL Toxicon 26:34-34 (1988).
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 DR PIR; B26744; B26744.
 DR GO; GO:0005615; C:extracellular space; IDA.

DR GO: GO:0045776; P:negative regulation of blood pressure; ISS.
DR GO: GO:0045987; P:positive regulation of smooth muscle contra. . . ; TAS.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAXININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 31.1%; Score 23; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
|||
DB 2 PPGFTP 7

RESULT 6

ID GRAR_RANRU STANDARD; PRT; 12 AA.
AC P40754;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Granuliberin-R.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP TISSUE=Skin secretion;
RX MEDLINE=78062810; PubMed=589733;
RA Nakajima T., Yasuhara T.;
RT "A new mast cell degranulating peptide, granuliberin-R, in the frog
RL Chem. Pharm. Bull. 25:2464-2465 (1977).
RN [2]

SYNTHESIS.

RX MEDLINE=78189201; PubMed=657408;
RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,
RA Koyama K., Yajima H.;
RT "Synthesis of the dodecapeptide amide corresponding to the entire
RT amino acid sequence of granuliberin-R, a new frog skin peptide from
RT Rana rugosa.";
RL Chem. Pharm. Bull. 26:1222-1230 (1978).
CC -!- FUNCTION: Mast cell degranulating peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Mast cell degranulation; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1424 MW; 23974EB9CA1B5047 CRC64;

Query Match 31.1%; Score 23; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PAYRPP 8
|||
DB 5 PIYRRP 10

RESULT 7

ID BRK_PARID STANDARD; PRT; 13 AA.
AC P42717;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Waspykinin.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Parapolybia.

OX NCBI_TaxID=31921;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of
RT Parapolybia indica.";
RL Eisei Dobutsu 39:105-111 (1988).

CC -!- FUNCTION: Induces smooth muscle contraction.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: Belongs to the bradykinin family.
KW Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1573 MW; 2673CB3D83ECC867 CRC64;

Query Match 31.1%; Score 23; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 7e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
|||
DB 5 PPGFSP 10

RESULT 8

ID BRK_ONCMY STANDARD; PRT; 10 AA.
AC Q9PRZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]

SEQUENCE

RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RT trout plasma.";
RL FEBS Lett. 334:75-78 (1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the bradykinin family.

DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.

SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 29.7%; Score 22; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
|||
DB 3 PPGWSP 8

RESULT 9

ID TY13_PHYRO STANDARD; PRT; 13 AA.
AC P04056;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaoidea; Hylidae;

OC Phyllomedusinae; Phyllomedusa.
 OX NCBI_TaxID=8394;
 RN [1]
 RP SEQUENCE.
 RA Montecucchi P.C., Gozzini L., Ersamer V.;
 RT "Primary structure determination of a tryptophan-containing
 RL tripeptide from Phyllomedusa rohdei".
 RL Int. J. Pept. Protein Res. 27:175-182(1986).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; A05174; A05174.
 KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
 FT MOD RES 1
 FT MOD RES 1
 FT MOD RES 1
 SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;
 Query Match 29.7%; Score 22; DB 1; Length 13;
 Best Local Similarity 40.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 3 PAYRPPNAPI 12
 DB 4 PWWPPPIYPM 13
 RESULT 10
 ID OVM LEPDE STANDARD; PRT; 6 AA.
 AC P42985;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Oviductal motility stimulating peptide (Leb-OVM).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytaphaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 EX MEDLINE=91271080; PubMed=2052497;
 RA Spittels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
 RA Proost P., Torrekens S., de Loof A.;
 RT "Isolation, identification and synthesis of novel oviductal motility
 RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
 RL decemlineata".
 RL Peptides 12:31-36(1991).
 CC -!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
 CC oviduct.
 KW Neuropeptide; Amidation.
 FT MOD RES 6
 FT MOD RES 6
 FT MOD RES 6
 SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;
 Query Match 27.0%; Score 20; DB 1; Length 6;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 AYRP 7
 DB 2 AYKP 5
 RESULT 11
 ID TWOF_AEDAE STANDARD; PRT; 10 AA.
 AC P19425;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Tryptsin-modulating oostatic factor (TWOF) (COSH).
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
 OX NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE.
 RA STRAIN=Vero beach; TISSUE=Ovary;
 RX MEDLINE=90367888; PubMed=2394318;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mosquito oostatic factor: a novel decapeptide modulating
 RT trypsin-like enzyme biosynthesis in the midgut".
 RL FASEB J. 4:3015-3020(1990).
 RN [2]
 RP SEQUENCE.
 RX STRAIN=Vero beach; TISSUE=Ovary;
 RX MEDLINE=93357794; PubMed=8353526;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mass spectrometry and characterization of Aedes aegypti trypsin
 RT modulating oostatic factor (TWOF) and its analogs".
 RL Insect Biochem. Mol. Biol. 23:703-712(1993).
 CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
 CC in the midgut which indirectly reduces the vitellogenin
 CC concentration in the hemolymph resulting in inhibition of oocyte
 CC development.
 CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
 CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at
 CC 36 hrs and stops at 56 hrs.
 DR PIR; A36454; A36454.
 KW Hormone.
 FT VARIANT 3 10 POLY-PRO.
 FT VARIANT 1 2 YD -> DY (IN TWOF(B)).
 SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;
 Query Match 27.0%; Score 20; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 PAYRPP 8
 DB 3 PAPPPP 8
 RESULT 12
 ID NEUU_CAVPO STANDARD; PRT; 9 AA.
 AC P34966;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuromedin U-9 (NMU-9).
 GN NMU.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Small intestine;
 RX MEDLINE=90341105; PubMed=2381877;
 RA Murphy R., Turner C.A., Furness J.B., Parker L., Gitaud A.;
 RT "Isolation and microsequence analysis of a novel form of neuromedin U
 RT from guinea pig small intestine".
 RL Peptides 11:613-617(1990).
 CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes
 CC selective vasoconstriction.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the NmU family.
 DR InterPro; IPR008199; NMU.
 DR Pfam; PF02070; NMU; 1.
 DR PROSITE; PS00967; NMU; 1.
 KW Amidation; Hormone.
 FT MOD RES 9
 FT MOD RES 9
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1169 MW; 1ECF177409C729DB CRC64;
 Query Match 25.7%; Score 19; DB 1; Length 9;

Best Local Similarity 60.0%; Pred. No. 1.4e+05; Mismatches 1; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 YRPN 9
: || |
5 FRPN 9

Db

RESULT 13
BPP8_BOTIN STANDARD; PRT; 10 AA.
ID BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).
DE Bothrops insularis (Island jararaca) (Queimada jararaca).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.
CC PIR; H37196; H37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 25.7%; Score 19; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2e+03; Mismatches 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PNAP 11
: || |
6 PNIP 9

Db

RESULT 14
URE3_MORNO STANDARD; PRT; 10 AA.
ID URE3_MORNO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit) (Urease 6 kDa subunit) (Fragment).
DE UREA.
GN Morganella morganii (Proteus morganii).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson B.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and isolation of gene sequences."
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the urease gamma subunit family.

DR PIR; C35389; C35389.
DR HAMAP; MF_00739; -; 1.
KW Hydrolase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 25.7%; Score 19; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPP 3
: || |
4 TPP 6

Db

RESULT 15
PARI_CALVO STANDARD; PRT; 12 AA.
ID PARI_CALVO STANDARD; PRT; 12 AA.
AC P41889;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Callimyrinamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duvé H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I., Renfield J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated callimyrinamides) from the blowfly Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: Belongs to the PARP (FMRamide related peptide) family.
DR PIR; E44787; E44787.
KW Neuropeptide; Amidation.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match 25.7%; Score 19; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.4e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PNAP 11
: || |
2 PNQP 5

Db

Search completed: August 9, 2004, 18:34:58
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:30:25 ; Search time 34 Seconds
(without alignments)
120.639 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPPAYRPPNAPIL 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3001

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	35.1	11	11 Q80W11	Q80w11 mus sp. nt-
2	25	33.8	10	4 Q3UE86	Q3ue86 homo sapien
3	23	31.1	12	13 Q9PSW5	Q9psw5 gallus gall
4	22	29.7	9	4 Q9UCS8	Q9ucs8 homo sapien
5	22	29.7	9	10 P82429	P82429 nicotiana t
6	22	29.7	9	13 Q9PRJ4	Q9prj4 lepisosteus
7	21.5	29.1	12	10 P82441	P82441 nicotiana t
8	21	28.4	11	6 Q9GL48	Q9gl48 sus scrofa
9	21	28.4	13	4 Q9UDC5	Q9udc5 homo sapien
10	21	28.4	13	10 Q43174	Q43174 solanum tub
11	21	28.4	13	12 P90442	P90442 spodoptera
12	20	27.0	10	2 Q9RJF1	Q9rjf1 pseudomonas
13	20	27.0	12	5 Q61574	Q61574 osteragla
14	20	27.0	12	11 Q80XV4	Q80xv4 rattus sp.
15	20	27.0	12	11 Q64313	Q64313 rattus norv
16	20	27.0	13	12 Q67604	Q67604 squash leaf

ALIGNMENTS

RESULT 1

Q80W11 ID Q80W11 PRELIMINARY; PRT; 11 AA.

AC Q80W11; DT 01-JUN-2003 (T-EMBLrel. 24, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE NT-3 transcript A (Fragment).

GN NT-3.

OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10095;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95040015; PubMed=7952296;

RA Leingartner A., Lindholm D.;

RT "Two promoters direct transcription of the mouse NT-3 gene.";

RL Eur. J. Neurosci. 6:1149-1159(1994).

DR EMBL; S75812; AAP31855.1; -.

FT NON TER 11

SQ SEQUENCE 11 AA; 1348 MW; 2280047D0DC5A777 CRC64;

Query Match. 35.1%; Score 26; DB 11; Length 11;

Best Local Similarity 44.4%; Pred. No. 1e+03; Mismatches 4; Indels 0; Gaps 0;

Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 5 YRPPNAPIL 13

Db 2 WQPPSARIM 10

RESULT 2

Q9UE86 ID Q9UE86 PRELIMINARY; PRT; 10 AA.

AC Q9UE86;

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

Q82622 avian infec
Q8cje0 rattus norv
Q9QW9 polyomaviru
Q8jv70 polyomaviru
Q9QW1 polyomaviru
Q8jv68 polyomaviru
Q9Q348 hepatitis g
Q9QW9 polyomaviru
Q9QW7 polyomaviru
Q8jv66 polyomaviru
Q9QV7 polyomaviru
Q8jv82 polyomaviru
Q8jv76 polyomaviru
Q9QW5 polyomaviru
Q9QW3 polyomaviru
Q9QW5 polyomaviru
Q8jv80 polyomaviru
Q9QX1 polyomaviru
Q9QX9 polyomaviru
Q8jv72 polyomaviru
Q86324 rous sarcom
Q86325 rous sarcom
Q86326 rous sarcom
Q8jv98 homo sapien
Q9ttc0 gorilla gor
P82328 pisum sativ
Q50476 mycobacteri

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DE Collagen alpha 1(I) chain (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92042176; PubMed=193261;
RA Hawkins J.R., Superfi-Furga A., Steinmann B., Dalglish R.;
RT "A 9-base pair deletion in COL1A1 in a lethal variant of osteogenesis
RT imperfecta";
RL J. Biol. Chem. 266:22370-22374(1991).
DR EMBL; S66556; AAB20361.1; -.
DR GO; GO:0005584; C:collagen type I; NAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
DR GO; GO:0007155; P:cell adhesion; NAS.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 777 MW; 2D20F6D8676DD867 CRC64;

Query Match 33.8%; Score 25; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPNAP 11
DB 2 PPGAP 6

RESULT 3
Q9PSW5 PRELIMINARY; PRT; 12 AA.
AC Q9PSW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE I kappa B-alpha (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96125200; PubMed=8543172;
RA Krishnan V.A., Schazle J.D., Hinojos C.M., Bose H.R. Jr.;
RT "Structure and regulation of the gene encoding avian inhibitor of
RT nuclear factor kappa B-alpha.";
RL Gene 166:261-266(1995).
DR EMBL; L27342; AAA92641.1; -.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1276 MW; E584F64824C77401 CRC64;

Query Match 31.1%; Score 23; DB 13; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 AYRPPNAP 11
DB 4 AHRPAEPP 11

RESULT 4
Q9UCS8 PRELIMINARY; PRT; 9 AA.
AC Q9UCS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92075598; PubMed=1742316;
RA Ehnholm C., Bozas S.E., Tenkanen H., Kirsbaum L., Matso J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT protein of human blood are different proteins which both bind to
RT apolipoprotein A-I.";
RL Biochim. Biophys. Acta 1086:255-260(1991).
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005319; F:lipid transporter activity; NAS.
DR GO; GO:0008203; P:cholesterol metabolism; ISS.
DR GO; GO:0008669; P:lipid transport; ISS.
FT NON_TER 1
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 981 MW; 7F837775A6C7776B CRC64;

Query Match 29.7%; Score 22; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPNAP 11
DB 3 PPGSP 7

RESULT 5
P82429 PRELIMINARY; PRT; 9 AA.
AC P82429;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 44 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RA STRAIN=CV. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 986 MW; C22CCAAADC6C77776 CRC64;

Query Match 29.7%; Score 22; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 RPPNAPIL 13
DB 2 QPPQADFL 9

RESULT 6
Q9PRJ4 PRELIMINARY; PRT; 9 AA.
AC Q9PRJ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Bradykinin.

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OS Lepisosteus osseus (Long-nosed gar), and
OS Amla calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus.
OX NCBI_TaxID=34771, 7924;
RN [1]
RP SEQUENCE.
RX MEDLINE=95390361; PubMed=7651903;
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [Trp]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar.";
RL Peptides 16:485-489 (1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;

Query Match 29.7%; Score 22; DB 13; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
Db |||:|
2 PPGWSP 7

RESULT 7
P82441 PRELIMINARY; PRT; 12 AA.
AC P82441
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 26 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA.
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -|- SUBCELLULAR LOCATION: CELL WALL.
CC -|- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1234 MW; 340012240872C9D7 CRC64;

Query Match 29.1%; Score 21.5; DB 10; Length 12;
Best Local Similarity 41.7%; Pred. No. 5.6e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 1 TPPAYRPENAPI 12
Db |||:|:|
1 SPPE---PFVPV 9

RESULT 8
Q9GL48 PRELIMINARY; PRT; 11 AA.
AC Q9GL48
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein-coupled receptor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
```

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OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagasaka T., Bouliday G., Coupel S., Coulon F., Tesson L.,
RA Heslan J.-M., Soullieu J.-P., Charreau B.;
RT "Alternative double screening for differentially expressed genes by
RT modified RNA differential display and semi-quantitative Reverse
RT Northern blot.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF319662; AAG33870.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1298 MW; 822261F10861BB41 CRC64;

Query Match 28.4%; Score 21; DB 6; Length 11;
Best Local Similarity 75.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPAY 5
Db |||
2 PPTY 5

RESULT 9
Q9UDC6 PRELIMINARY; PRT; 13 AA.
AC Q9UDC6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ENDOTHELIUM-derived RELATING factor, nitric oxide synthase
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054573; PubMed=13955404;
RA Janssens S.P., Simouchi A., Quartermous T., Bloch D.B., Bloch K.D.;
RT "Cloning and expression of a cDNA encoding human endothelium-derived
RT relating factor/nitric oxide synthase.";
RL J. Biol. Chem. 267:22694-22694(1992).
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1390 MW; 3231B6DFEC7BB867 CRC64;

Query Match 28.4%; Score 21; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 7.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 4 AVRPP---NAP 11
Db |||:|:|
2 AFDPPGSDTNSP 13

RESULT 10
Q43174 PRELIMINARY; PRT; 13 AA.
AC Q43174
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-fructofuranosidase (EC 3.2.1.26) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Cara;
```


RL J. Biol. Chem. 268:22164-22169(1993).

DR EMBL; S66180; AAF13974.1; -.

SQ SEQUENCE 12 AA; 1436 MW; D33C6D2A83B36776 CRC64;

Query Match 27.0%; Score 20; DB 11; Length 12;

Best Local Similarity 60.0%; Pred. No. 9.7e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PPNAP 11

Db 2 PPROP 6

RESULT 15

Q64313

ID Q64313 PRELIMINARY; PRT; 12 AA.

AC Q64313;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN ENK.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_taxID=10116;

EN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Fisher 344; TISSUE=Striatum;

RX MEDLINE=90066445; PubMed=2573832;

RA Garrett J.E., Collard M.W., Douglass J.O.;

RT "Translational control of germ cell-expressed mRNA imposed by

alternative splicing: opioid peptide gene expression in rat testis."

EL Mol. Cell. Biol. 9:4381-4389(1989).

DR EMBL; K02805; AAA60733.1; -.

KW Hypothetical protein.

SQ SEQUENCE 12 AA; 1436 MW; D33C6D2A83B36776 CRC64;

Query Match

Best Local Similarity 27.0%; Score 20; DB 11; Length 12;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PPNAP 11

Db 2 PPROP 6

Search completed: August 9, 2004, 18:35:43.

Job time : 35 secs

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